GenCore version 4.5

OM protein - protein search, using sw model

Run on: October 4, 2002, 07:36:20 ; Search time 35.72 Seconds
(without alignments)
2857.694 Million cell updates/sec

Title: US-08-153-397A-2
Perfect score: 4928
Sequence: 1 MGPEALSSLLLLLLVASGDA.....QRPPFSQLHRFLAEDALNTV 919

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*
1: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:*
6: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*
7: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*
8: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*
9: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1988.DAT:*
10: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*
11: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
12: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
13: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:*
14: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*
15: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1994.DAT:*
16: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
17: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT:*
18: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1997.DAT:*
19: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4928	100.0	919	18	AAW34672	Human mammary carc
2	4921	99.9	919	16	AAR75502	Human mammary carc
3	4921	99.9	919	16	AAR75504	Human mammmary car
4	4844.5	98.3	914	16	AAR71100	Protein-tyrosine-k
5	4697.5	95.3	882	18	AAW34673	Human mammary carc
6	4656.5	94.5	876	18	AAW34675	Human mammary carc
7	3298	66.9	624	21	AAB54286	Human pancreatic c
8	3298	66.9	624	22	AAG73767	Human colon cancer
9	3003	60.9	563	18	AAW34674	Human mammary carc
10	2404	48.8	855	16	AAR75503	Human colonic aden
11	2404	48.8	855	16	AAR75505	Human colonic aden
12	2404	48.8	855	18	AAW34671	CCK-2, a human mam
13	2404	48.8	855	19	AAW77114	Discoidin domain r
14	2402	48.7	854	19	AAW79152	Receptor protein t
15	2402	48.7	854	20	AAW81409	Receptor protein t
16	2254	45.7	904	22	AAM25564	Human protein sequ
17	1814	36.8	650	15	AAR54089	Partial sequence o
18	645	13.1	822	16	AAR81630	Human trkB recepto
19	645	13.1	822	21	AAY51599	Human trkB recepto
20	645	13.1	847	16	AAW11941	gD.trkB fusion use
21	641.5	13.0	825	20	AAY06595	Neurotrophin-3 rec
22	640.5	13.0	825	16	AAR81631	Human trkC recepto
23	640.5	13.0	850	16	AAW11942	gD.trkC fusion use
24	628	12.7	790	20	AAY26956	Human TrkA protein
25	627	12.7	790	21	AAY51603	Human trk receptor
26	627	12.7	814	16	AAW11940	gD.trkA fusion use
27	627	12.7	830	16	AAR81627	Human trkC recepto
28	624.5	12.7	825	15	AAR62021	Porcine TrkC prote
29	623.5	12.7	839	16	AAR81625	Human trkC recepto
30	623.5	12.7	839	21	AAY51601	Human trkC recepto
31	621.5	12.6	825	13	AAR27148	Adult porcine trkC
32	621.5	12.6	825	14	AAR30883	trkC gene prod. S
33	615	12.5	503	22	ABG20277	Novel human diagno
34	609	12.4	728	13	AAR27149	Mouse trkC proto-o
35	609	12.4	728	14	AAR30884	Partial trkC gene
36	609	12.4	728	15	AAR62022	Murine TrkC protei
37	607.5	12.3	268	20	AAY43975	Human protein kina
38	607.5	12.3	839	15	AAR71621	Porcine TrkC K2 is
39	603.5	12.2	739	15	AAR71618	Murine TrkC K3 iso
40	593.5	12.0	868	18	AAW26610	Rat muscle-specifi
41	593.5	12.0	868	18	AAW26507	Rat Dmk receptor.
42	592.5	12.0	881	17	AAR84091	Nsk2 receptor with
43	590	12.0	867	19	AAW62583	Mouse receptor tyr
44	590	12.0	868	17	AAR92717	Mouse muscle-local
45	590	12.0	871	17	AAR84087	Nsk2 receptor. Mu

ALIGNMENTS

RESULT 1
AAW34672
ID AAW34672 standard; Protein; 919 AA.
XX
AC AAW34672;
XX
DT 17-FEB-1998 (first entry)
XX
DE Human mammary carcinoma kinase 10 (MCK-10) amino acid sequence.
XX
KW Mammary carcinoma kinase; MCK-10; receptor tyrosine kinase;
KW proliferative disease; cancer; insulin receptor family;
KW tyrosine kinase neurotropin receptor; MCK-10 activity;
KW neurological disorder; aberrant expression.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1..18
FT		/label= signal_sequence
FT	Protein	19..919
FT		/note= "mature_protein"
FT	Domain	31..185
FT		/label= Discoidin_I_like_domain
FT	Cleavage-site	304..307
FT		/label= endopeptidase_furin
FT		/note= "putative precursor cleavage site"
FT	Region	48..439
FT		/label= transmembrane_region
FT	Binding-site	617..627
FT		/label= ATP_binding_motif
FT	Modified-site	802..803
FT		/label= autophosphorylation_sites
FT		/note= "putative"

```
FT   Modified-site   798
FT                   /label= autophosphorylation_site
FT                   /note= "putative"
FT   Binding-site    844..847
FT                   /label= binding_motif_for_P13_kinase
FT                   /note= "binding motif for phosphatidylinositol 3'
FT                        kinase"
FT   Binding-site    832..832
FT                   /label= potential_substrate_binding_site
FT   Binding-site    506..509
FT                   /label= putative_receptor_binding_site_for_SHC
FT                   /note= "SHC is an oncogenic SH2 domain containing
FT                        molecule"
FT   Binding-site    510..513
FT                   /label= GTPase_activity_protein_binding_site
FT                   /note= "putative"
FT   Region          505..541
FT                   /note= "alternatively spliced variant"
FT   Region          666..671
FT                   /note= "alternatively spliced sequence"
FT   Region          26..42
FT                   /note= "antibody recognition sequence NTalpha"
FT   Region          309..321
FT                   /note= "antibody recognition sequence NTbeta"
FT   Region          902..919
FT                   /note= "antibody recognition sequence CTbeta"
XX
PN   US5677144-A.
XX
PD   14-OCT-1997.
XX
PF   08-NOV-1994;   94US-0336343.
XX
PR   16-NOV-1993;   93US-0153397.
XX
PA   (ALVE/) ALVES F H E.
PA   (ULLR/) ULLRICH A.
XX
PI   Alves FHE,  Ullrich A;
XX
DR   WPI; 1997-511869/47.
DR   N-PSDB; AAT93785.
XX
PT   Truncated receptor tyrosine kinase CCK-2 - and nucleic acid coding
PT   for it, useful for cancer diagnosis
XX
PS   Disclosure; Fig 1; 70pp; English.
XX
CC   The present sequence represents the protein sequence of a mammary
CC   carcinoma kinase, called MCK-10. This kinase belongs to a novel family
CC   of receptor tyrosine kinases, and expression is associated with
CC   proliferative diseases such as cancer. The MCK-10 receptor tyrosine
CC   kinase has extensive sequence similarity to the insulin receptor family.
CC   The MCK-10 gene was isolated by PCR using 2 degenerate oligonucleotide
CC   primer pools, using a template cDNA synthesised by reverse transcription
CC   of poly-A RNA from the human mammary carcinoma cell line MCF7. The MCK-10
CC   protein contains 2 alternative spliced sequences, from amino acids
CC   505-541 and 666-671. The sequence represented by amino acids 585-595 may
CC   be important, as deletion of this motif in the activin receptor
CC   serine/threonine kinase results in reduced ligand binding affinity.
CC   MCK-10 is expressed in brain tissue, and the protein shares homology with
CC   the tyrosine kinase neurotropin receptor. Modulation of MCK-10 activity
CC   therefore may be used for treatment of neurological disorders. MCK-10 is
CC   also expressed in a variety of cancer cell lines and tumour tissue. The
CC   nucleotide sequence of MCK-10, or parts of it, can be used for diagnostic
CC   purposes to detect aberrant expression of MCK-10 genes. Inhibitors of
CC   MCK-10 receptor activity may have therapeutic value in the treatment of
CC   diseases such as cancer.
XX
SQ   Sequence   919 AA;
```

Query Match 100.0%; Score 4928; DB 18; Length 919;

```
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  919;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MGPEALSSLLLLLLVASGDADMKGHFDPAKCRYALGMQDRTIPDSDISASSSWSDSTAAR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mgpealssllllllvasgdadmkghfdpakcryalgmqdrtipdsdisassswsdstaar 60

Qy      61 HSRLESSDGDGAWCPAGSVFPKEEEYLQVDLQRLHLVALVGTQGRHAGGLGKEFSRSYRL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 hsrlessdgdgawcpagsvfpkeeeylqvdlqrlhlvalvgtqgrhagglgkefsrsyrl 120

Qy     121 RYSRDGRRWMGWKDRWGQEVISGNEDPEGVVLKDLGPPMVARLVRFYPRADRVMSVCLRV 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 rysrdgrrwmgwkdrwgqevisgnedpegvvlkdlgppmvarlvrfypradrvmsvclrv 180

Qy     181 ELYGCLWRDGLLSYTAPVGQTMYLSEAVYLNDSTYDGHTVGGLQYGGLGQLADGVVGLDD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 elygclwrdgllsytapvgqtmylseavylndstydghtvgglqygglgqladgvvgldd 240

Qy     241 FRKSQELRVWPGYDYVGWSNHSFSSGYVEMEFEFDRLRAFQAMQVHCNNMHTLGARLPGG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 frksqelrvwpgydyvgwsnhsfssgyvemefefdrlrafqamqvhcnnmhtlgarlpgg 300

Qy     301 VECRFRRGPAMAWEGEPMRHNLGGNLGDPRARAVSVPLGGRVARFLQCRFLFAGPWLLFS 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 vecrfrrgpamawegepmrhnlggnlgdpraravsvplggrvarflqcrflfagpwllfs 360

Qy     361 EISFISDVVNNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTAILI 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 eisfisdvvnnsspalggtfppapwwppgppptnfssleleprgqqpvakaegsptaili 420

Qy     421 GCLVAIILLLLLIIALMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTILINNRPGPRE 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 gclvaiilllllliialmlwrlhwrrllskaerrvleeeltvhlsvpgdtilinnrpgpre 480

Qy     481 PPPYQEPRPRGNPPHSAPCVPNGSALLLSNPAYRLLLATYARPPRGPGPPTPAWAKPTNT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 pppyqeprprgnpphsapcvpngsalllsnpayrlllatyarpprgpgpptpawakptnt 540

Qy     541 QAYSGDYMEPEKPGAPLLPPPPQNSVPHYAEADIVTLQGVTGGNTYAVPALPPGAVGDGP 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 qaysgdymepekpgapllppppqnsvphyaeadivtlqgvtggntyavpalppgavgdgp 600

Qy     601 PRVDFPRSRLRFKEKLGEGQFGEVHLCEVDSPQDLVSLDFPLNVRKGHPLLVAVKILRPD 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 prvdfprsrlrfkeklgegqfgevhlcevdspqdlvsldfplnvrkghpllvavkilrpd 660

Qy     661 ATKNASFSLFSRNDFLKEVKIMSRLKDPNIIRLLGVCVQDDPLCMITDYMENGDLNQFLS 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 atknasfslfsrndflkevkimsrlkdpniirllgvcvqddplcmitdymengdlnqfls 720

Qy     721 AHQLEDKAAEGAPGDGQAAQGPTISYPMLLHVAAQIASGMRYLATLNFVHRDLATRNCLV 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ahqledkaaegapgdgqaaqgptisypmllhvaaqiasgmrylatlnfvhrdlatrnclv 780

Qy     781 GENFTIKIADFGMSRNLYAGDYYRVQGRAVLPIRWMAWECILMGKFTTASDVWAFGVTLW 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 genftikiadfgmsrnlyagdyyrvqgravlpirwmawecilmgkfttasdvwafgvtlw 840

Qy     841 EVLMLCRAQPFGQLTDEQVIENAGEFFRDQGRQVYLSRPPACPQGLYELMLRCWSRESEQ 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 evlmlcraqpfgqltdeqvienageffrdqgrqvylsrppacpqglyelmlrcwsreseq 900

Qy     901 RPPFSQLHRFLAEDALNTV 919
           ||||||||||||||||||
Db     901 rppfsqlhrflaedalntv 919


RESULT   2
AAR75502
ID   AAR75502 standard; Protein; 919 AA.
XX
AC   AAR75502;
```

```
XX
DT   26-NOV-1995  (first entry)
XX
DE   Human mammary carcinoma kinase 10 (MCK-10).
XX
KW   Mammary carcinoma kinase 10; transmembrane receptor;
KW   receptor tyrosine kinase; cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..18
FT                   /label= signal
FT   Domain          31..185
FT                   /label= discoidin I-like domain
FT   Cleavage-site   304..307
FT                   /label= putative precursor cleavage site
FT   Region          417..439
FT                   /label= transmembrane
FT   Misc-difference 505..541
FT                   /label= alternatively spliced sequence I
FT   Misc-difference 666..671
FT                   /label= alternatively spliced sequence II
FT   Misc-difference 25..42
FT                   /label= NT alpha
FT                   /note= "peptide antibody recognition site"
FT   Misc-difference 309..321
FT                   /label= NT beta
FT                   /note= "see above"
FT   Misc-difference 909..919
FT                   /label= CT beta
FT                   /note= "see above"
XX
PN   WO9514088-A.
XX
PD   26-MAY-1995.
XX
PF   16-NOV-1994;   94WO-EP03797.
XX
PR   16-NOV-1993;   93US-0153397.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Alves FHE,  Ullrich A;
XX
DR   WPI; 1995-224054/29.
DR   N-PSDB; AAQ92520.
XX
PT   New nucleic acid encoding MCK-10 receptor tyrosine kinase - and
PT   derived vectors, transformed cells, proteins and antibodies useful
PT   for diagnosis and treatment of proliferative disease, esp. cancer,
PT   and for screening modulators
XX
PS   Disclosure; Page 53-55; 115pp; English.
XX
CC   cDNA prepd. from human breast cancer cell line MCF7 (ATCC HTB22) and
CC   used in a PCR with two degenerate oligo primer pools based on
CC   conserved sequences of the kinase domain of receptor tyrosine
CC   kinases. One clone, designated MCK-10, was identified as novel RTK.
CC   The PCR fragment was used to screen a lambda gt11 library of human
CC   fetal brain cDNA. Several overlapping clones were identified. The
CC   composite of these cDNA clones is given in AAQ92520 and the deduced AA
CC   sequence in AAR75502. Some of the clones had a deletion of 6 AAs at
CC   posn. 2315 in the MCK-10 sequence. MCK-10 has all the
CC   characteristics of a receptor PTK (see AAR75502 FT). Screening of
CC   human placental library yielded two cDNA clones MCK-10-1 and
CC   MCK-10-2. One of the clones isolated from the human fetal brain
CC   library contd. an additional 18 nts in the TK domain. The MCK-10 splice
CC   isoforms have been designated MCK-10-1 (with an additional 111 bp
CC   between nts 1832 and 1943); MCK-10-2 (without any insertions); MCK-10-3
CC   (with the additional 111 bp and and 18 bp in the TK domain); and MCK10-4
CC   (with the additional 18 bp). The predicted mol. wts. of MCK-10-1 and
CC   MCK-10-2 proreceptors are 101.13 and 97.17 kD respectively, and can thus
CC   be subdivided into a 34.31 kD alpha subunit and and 66.84 or 62.88 kD
CC   beta subunits that contain the TK homology and alternative splice sites.
XX
SQ   Sequence   919 AA;


  Query Match             99.9%;  Score 4921;  DB 16;  Length 919;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MGPEALSSLLLLLLVASGDADMKGHFDPAKCRYALGMQDRTIPDSDISASSSWSDSTAAR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mgpealssllllllvasgdadmkghfdpakcryalgmqdrtipdsdisassswsdstaar 60

Qy      61 HSRLESSDGDGAWCPAGSVFPKEEEYLQVDLQRLHLVALVGTQGRHAGGLGKEFSRSYRL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 hsrlessdgdgawcpagsvfpkeeeylqvdlqrlhlvalvgtqgrhagglgkefsrsyrl 120

Qy     121 RYSRDGRRWMGWKDRWGQEVISGNEDPEGVVLKDLGPPMVARLVRFYPRADRVMSVCLRV 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 rysrdgrrwmgwkdrwgqevisgnedpegvvlkdlgppmvarlvrfypradrvmsvclrv 180

Qy     181 ELYGCLWRDGLLSYTAPVGQTMYLSEAVYLNDSTYDGHTVGGLQYGGLGQLADGVVGLDD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 elygclwrdgllsytapvgqtmylseavylndstydghtvgglqygglgqladgvvgldd 240

Qy     241 FRKSQELRVWPGYDYVGWSNHSFSSGYVEMEFEFDRLRAFQAMQVHCNNMHTLGARLPGG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 frksqelrvwpgydyvgwsnhsfssgyvemefefdrlrafqamqvhcnnmhtlgarlpgg 300

Qy     301 VECRFRRGPAMAWEGEPMRHNLGGNLGDPRARAVSVPLGGRVARFLQCRFLFAGPWLLFS 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 vecrfrrgpamawegepmrhnlggnlgdpraravsvplggrvarflqcrflfagpwllfs 360

Qy     361 EISFISDVVNNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTAILI 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 eisfisdvvnnsspalggtfppapwwppgppptnfssleleprgqqpvakaegsptaili 420

Qy     421 GCLVAIILLLLLIIALMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTILINNRPGPRE 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 gclvaiilllliialmlwrlhwrrllskaerrvleeeltvhlsvpgdtilinnrpgpre 480

Qy     481 PPPYQEPRPRGNPPHSAPCVPNGSALLLSNPAYRLLLATYARPPRGPGPPTPAWAKPTNT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 pppyqeprprgnpphsapcvpngsalllsnpayrlllatyarpprgpgpptpawakptnt 540

Qy     541 QAYSGDYMEPEKPGAPLLPPPPQNSVPHYAEADIVTLQGVTGGNTYAVPALPPGAVGDGP 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 qaysgdymepekpgapllppppqnsvphyaeadivtlqgvtggntyavpalppgavgdgp 600

Qy     601 PRVDFPRSRLRFKEKLGEGQFGEVHLCEVDSPQDLVSLDFPLNVRKGHPLLVAVKILRPD 660
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     601 prvdfprsrlrfkeklgegqfgevhlcevdspqhlvsldfplnvrkghpllvavkilrpd 660

Qy     661 ATKNASFSLFSRNDFLKEVKIMSRLKDPNIIRLLGVCVQDDPLCMITDYMENGDLNQFLS 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 atknasfslfsrndflkevkimsrlkdpniirllgvcvqddplcmitdymengdlnqfls 720

Qy     721 AHQLEDKAAEGAPGDGQAAQGPTISYPMLLHVAAQIASGMRYLATLNFVHRDLATRNCLV 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ahqledkaaegapgdgqaaqgptisypmllhvaaqiasgmrylatlnfvhrdlatrnclv 780

Qy     781 GENFTIKIADFGMSRNLYAGDYYRVQGRAVLPIRWMAWECILMGKFTTASDVWAFGVTLW 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 genftikiadfgmsrnlyagdyyrvqgravlpirwmawecilmgkfttasdvwafgvtlw 840

Qy     841 EVLMLCRAQPFGQLTDEQVIENAGEFFRDQGRQVYLSRPPACPQGLYELMLRCWSRESEQ 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 evlmlcraqpfgqltdeqvienageffrdqgrqvylsrppacpqglyelmlrcwsreseq 900

Qy     901 RPPFSQLHRFLAEDALNTV 919
           ||||||||||||||||||
Db     901 rppfsqlhrflaedalntv 919
```

```
RESULT  3
AAR75504
ID   AAR75504 standard; Protein; 919 AA.
XX
AC   AAR75504;
XX
DT   26-NOV-1995  (first entry)
XX
DE   Human mammmary carcinoma kinase 10 (MCK-10).
XX
KW   Mammary carcinoma kinase 10; MCK-10; transmembrane receptor;
KW   receptor tyrosine kinase; cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..18
FT                   /label= signal
FT   Domain          31..185
FT                   /label= discoidin I-like domain
FT   Cleavage-site   304..307
FT                   /label= putative precursor cleavage site
FT   Region          417..439
FT                   /label= transmembrane
FT   Misc-difference 505..541
FT                   /label= alternatively spliced sequence I
FT   Misc-difference 666..671
FT                   /label= alternatively spliced sequence II
FT   Misc-difference 25..42
FT                   /label= NT alpha
FT                   /note= "peptide antibody recognition site"
FT   Misc-difference 309..321
FT                   /label= NT beta
FT                   /note= "see above"
FT   Misc-difference 909..919
FT                   /label= CT beta
FT                   /note= "see above"
XX
PN   WO9514089-A.
XX
PD   26-MAY-1995.
XX
PF   16-NOV-1994;   94WO-EP03799.
XX
PR   16-NOV-1993;   93US-0153397.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Alves FHE,  Ullrich A;
XX
DR   WPI; 1995-224055/29.
DR   N-PSDB; AAQ92522.
XX
PT   New nucleic acid encoding CCK-2 receptor tyrosine kinase - and
PT   derived vectors, transformed cells, proteins and antibodies, useful
PT   for diagnosis and treatment of proliferative and nervous system
PT   diseases and for screening modulators
XX
PS   Disclosure; Page 70-72; 115pp; English.
XX
CC   cDNA prepd. from human breast cancer cell line MCF7 (ATCC HTB22) was
CC   used in a PCR with two degenerate oligo primer pools based on
CC   conserved sequences of the kinase domain of receptor tyrosine
CC   kinases. One clone, designated MCK-10, was identified as novle RTK.
CC   The PCR fragment was used to screen a lambda gtl1 library of human
CC   fetal brain cDNA. Several overlapping clones were identified. The
CC   composite of these cDNA clones is given in AAQ92522 and the deduced AA
CC   sequence in AAR75504. Some of the clones had a deletion of 6AA at posn.
CC    2315 in the MCK-10 sequence. MCK-10 has all the characteristics of
CC   a receptor PTK (see AAR75504 FT). Screening of human placental library
CC   yielded two cDNA clones. One of the clones isolated from the human
CC   fetal brain library contained an additional 18 nts in the TK
CC   domain. The MCK-10 splice isoforms have been designated MCK-10-1
CC   (with an additional 111 bp between nts 1832 and 1943); MCK-10-2
CC   (without any insertions); MCK-10-3 (with the additional 111 bps and
CC   18 bp in the TK domain); and MCK-10-4 (with the additional 18 bp).
CC   The predicted mol. wts. of MCK-10-1 and MCK-10-2 proreceptors are
CC   101.13 and 97.17 kD respectively, and can thus be subdivided into a
CC   34.31 kD alpha subunit and a 66.84 or 62.88 kD beta subunits that
CC   contain the TK homology and alternative splice sites.
XX
SQ   Sequence   919 AA;


  Query Match           99.9%;  Score 4921;  DB 16;  Length 919;
  Best Local Similarity 99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 MGPEALSSLLLLLLVASGDADMKGHFDPAKCRYALGMQDRTIPDSDISASSSWSDSTAAR 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 mgpealssllllllvasgdadmkghfdpakcryalgmqdrtipdsdisassswsdstaar 60

Qy     61 HSRLESSDGDGAWCPAGSVFPKEEEYLQVDLQRLHLVALVGTQGRHAGGLGKEFSRSYRL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 hsrlessdgdgawcpagsvfpkeeeylqvdlqrlhlvalvgtqgrhagglgkefsrsyrl 120

Qy    121 RYSRDGRRWMGWKDRWGQEVISGNEDPEGVVLKDLGPPMVARLVRFYPRADRVMSVCLRV 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 rysrdgrrwmgwkdrwgqevisgnedpegvvlkdlgppmvarlvrfypradrvmsvclrv 180

Qy    181 ELYGCLWRDGLLSYTAPVGQTMYLSEAVYLNDSTYDGHTVGGLQYGGLGQLADGVVGLDD 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 elygclwrdgllsytapvgqtmylseavylndstydghtvgglqyggLgqladgvvgldd 240

Qy    241 FRKSQELRVWPGYDYVGWSNHSFSSGYVEMEFEFDRLRAFQAMQVHCNNMHTLGARLPGG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 frksqelrvwpgydyvgwsnhsfssgyvemefefdrlrafqamqvhcnnmhtlgarlpgg 300

Qy    301 VECRFRRGPAMAWEGEPMRHNLGGNLGDPRARAVSVPLGGRVARFLQCRFLFAGPWLLFS 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 vecrfrrgpamawegepmrhnlggnlgdpraravsvplggrvarflqcrflfagpwllfs 360

Qy    361 EISFISDVVNNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTAILI 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 eisfisdvvnnsspalggtfppapwwppgppptnfsslleleprgqqpvakaegsptaili 420

Qy    421 GCLVAIILLLLLIIALMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTILINNRPGPRE 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 gclvaiillllliialmlwrlhwrrllskaerrvleeeltvhlsvpgdtilinnrpgpre 480

Qy    481 PPPYQEPRPRGNPPHSAPCVPNGSALLLSNPAYRLLLATYARPPRGPGPPTPAWAKPTNT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 pppyqeprprgnpphsapcvpngsalllsnpayrlllatyarpprgpgpptpawakptnt 540

Qy    541 QAYSGDYMEPEKPGAPLLPPPPQNSVPHYAEADIVTLQGVTGGNTYAVPALPPGAVGDGP 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 qaysgdymepekpgapllppppqnsvphyaeadivtlqgvtggntyavpalppgavgdgp 600

Qy    601 PRVDFPRSRLRFKEKLGEGQFGEVHLCEVDSPQDLVSLDFPLNVRKGHPLLVAVKILRPD 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 prvdfprsrlrfkeklgegqfgevhlcevdspqhlvsldfplnvrkghpllvavkilrpd 660

Qy    661 ATKNASFSLFSRNDFLKEVKIMSRLKDPNIIRLLGVCVQDDPLCMITDYMENGDLNQFLS 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 atknasfslfsrndflkevkimsrlkdpniirllgvcvqddplcmitdymengdlnqfls 720

Qy    721 AHQLEDKAAEGAPGDGQAAQGPTISYPMLLHVAAQIASGMRYLATLNFVHRDLATRNCLV 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ahqledkaaegapgdgqaaqgptisypmllhvaaqiasgmrylatlnfvhrdlatrnclv 780

Qy    781 GENFTIKIADFGMSRNLYAGDYYRVQGRAVLPIRWMAWECILMGKFTTASDVWAFGVTLW 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 genftikiadfgmsrnlyagdyyrvqgravlpirwmawecilmgkfttasdvwafgvtlw 840
```

```
Qy    841 EVLMLCRAQPFGQLTDEQVIENAGEFFRDQGRQVYLSRPPACPQGLYELMLRCWSRESEQ 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 evlmlcraqpfgqltdeqvienageffrdqgrqvylsrppacpqglyelmlrcwsreseq 900

Qy    901 RPPFSQLHRFLAEDALNTV 919
          ||||||||||||||||||||
Db    901 rppfsqlhrflaedalntv 919


RESULT   4
AAR71100
ID   AAR71100 standard; Protein; 914 AA.
XX
AC   AAR71100;
XX
DT   17-AUG-1995  (first entry)
XX
DE   Protein-tyrosine-kinase PTK22.
XX
KW   Protein-tyrosine-kinase; PTK; discoidin domain receptor; cancer;
KW   breast tumor; mamma carcinoma; diagnosis; prognosis; therapy.
XX
OS   Homo sapiens.
XX
PN   WO9502187-A.
XX
PD   19-JAN-1995.
XX
PF   08-JUL-1994;   94WO-GB01480.
XX
PR   09-JUL-1993;   93GB-0014271.
XX
PA   (CANC-) CANCER RES INST.
PA   (WELL ) WELLCOME FOUND LTD.
XX
PI   Barker KT, Crompton MR, Gusterson BA, Martindale JE;
PI   Mitchell PJ, Page MJ, Spence P;
XX
DR   WPI; 1995-066991/09.
DR   N-PSDB; AAQ84782.
XX
PT   Method for screening substances, using protein tyrosine kinase -
PT   for potential utility as therapeutic agents for cancer
XX
PS   Disclosure; Page 26-30; 51pp; English.
XX
CC   cDNA derived from tumor metastatic tissue was amplified using
CC   primers (given in AAQ84783-84) based on sequences (AAR71101, AAR71103)
CC   associated with protein-tyrosine-kinases (PTK).  Novel PTK22 was
CC   identified in an isolated subclone.  The 3' sequence of PTK22 was
CC   obtained by reverse transcription (using the primer of AAQ84786) and
CC   PCR amplification (primers AAQ84787-88) of RNA of human breast
CC   carcinoma cell line MDA MG 468.  The partial DNA sequence of PTK22
CC   is given in AAQ84782.
XX
SQ   Sequence   914 AA;


  Query Match             98.3%;  Score 4844.5;  DB 16;  Length 914;
  Best Local Similarity   98.7%;  Pred. No. 0;
  Matches  908;  Conservative    1;  Mismatches    4;  Indels    7;  Gaps    2;

Qy      1 MGPEALSSLLLLLLVASGDADMKGHFDPAKCRYALGMQDRTIPDSDISASSSWSDSTAAR 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 mgpealssllllllvasgdadmkghfdpakcryalgmqdrtipdsdisassswsdstaar 60

Qy     61 HSRLESSDGDGAWCPAGSVFPKEEEYLQVDLQRLHLVALVGTQGRHAGGLGKEFSRSYRL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 hsrlessdgdgawcpagsvfpkeeeylqvdlqrlhlvalvgtqgrhagglgkefsrsyrl 120

Qy    121 RYSRDGRRWMGWKDRWGQEVISGNEDPEGVVLKDLGPPMVARLVRFYPRADRVMSVCLRV 180
          |||| |||||||||| |||||||||||||||||||||||||| ||||||||||||||||||
Db    121 rysrhgrrwmgwkdrwvqevisgnedpegvvlkdlgppmvarlvrlypradrvmsvclrv 180

Qy    181 ELYGCLWRDGLLSYTAPVGQTMYLSEAVYLNDSTYDGHTVGGLQYGGLGQLADGVVGLDD 240
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 elygclwrdgllyytapvgqtmylseavylndstydghtvgglqygglgqladgvvgldd 240

Qy    241 FRKSQELRVWPGYDYVGWSNHSFSSGYVEMEFEFDRLRAFQAMQVHCNNMHTLGARLPGG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 frksqelrvwpgydyvgwsnhsfssgyvemefefdrlrafqamqvhcnnmhtlgarlpgg 300

Qy    301 VECRFRRGPAMAWEGEPMRHNLGGNLGDPRARAVSVPLGGRVARFLQCRFLFAGPWLLFS 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 vecrfrrgpamawegepmrhnlggnlgdpraravsvplggrvarflqcrflfagpwllfs 360

Qy    361 EISFISDVVNNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQ-QPVAKAEGSPTAIL 419
          |||||||||||||||||||||||||||||||||||||||||||| :|||||||||||||||
Db    361 eisfisdvvnnsspalggtfppapwwppgppptnfsslelepr gqprpvakaegsptail 420

Qy    420 IGCLVAIILLLLLIIALMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTILINNRPGPR 479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 igclvaiilllliialmlwrlhwrrllskaerrvleeeltvhlsvpgdtilinnrpgpr 480

Qy    480 EPPPYQEPRPRGNPPHSAPCVPNGSALLLSNPAYRLLLATYARPPRGPGPPTPAWAKPTN 539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 epppyqeprprgnpphsapcvpngsalllsnpayrlllatyarpprgpgpptpawakptn 540

Qy    540 TQAYSGDYMEPEKPGAPLLPPPPQNSVPHYAEADIVTLQGVTGGNTYAVPALPPGAVGDG 599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 tqaysgdymepekpgapllppppqnsvphyaeadivtlqgvtggntyavpalppgavgdg 600

Qy    600 PPRVDFPRSRLRFKEKLGEGQFGEVHLCEVDSPQDLVSLDFPLNVRKGHPLLVAVKILRP 659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 pprvdfprsrlrfkeklgegqfgevhlcevdspqdlvsldfplnvrkghpllvavkilrp 660

Qy    660 DATKNASFSLFSRNDFLKEVKIMSRLKDPNIIRLLGVCVQDDPLCMITDYMENGDLNQFL 719
          ||||||      ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 datkna------rndflkevkimsrlkdpniirllgvcvqddplcmitdymengdlnqfl 714

Qy    720 SAHQLEDKAAEGAPGDGQAAQGPTISYPMLLHVAAQIASGMRYLATLNFVHRDLATRNCL 779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    715 sahqledkaaegapgdgqaaqgptisypmllhvaaqiasgmrylatlnfvhrdlatrncl 774

Qy    780 VGENFTIKIADFGMSRNLYAGDYYRVQGRAVLPIRWMAWECILMGKFTTASDVWAFGVTL 839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    775 vgenftikiadfgmsrnlyagdyyrvqgravlpirwmawecilmgkfttasdvwafgvtl 834

Qy    840 WEVLMLCRAQPFGQLTDEQVIENAGEFFRDQGRQVYLSRPPACPQGLYELMLRCWSRESE 899
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    835 wevlmlcraqpfgqltdeqvienageffrdqgrqvylsrppacpqglyelmlrcwsrese 894

Qy    900 QRPPFSQLHRFLAEDALNTV 919
          ||||||||||||||||||||
Db    895 qrppfsqlhrflaedalntv 914


RESULT   5
AAW34673
ID   AAW34673 standard; Protein; 882 AA.
XX
AC   AAW34673;
XX
DT   17-FEB-1998  (first entry)
XX
DE   Human mammary carcinoma kinase 10 (MCK-10) spice variant 1.
XX
KW   Mammary carcinoma kinase; MCK-10; receptor tyrosine kinase;
KW   proliferative disease; cancer; insulin receptor family;
KW   tyrosine kinase neurotropin receptor; MCK-10 activity;
KW   neurological disorder; aberrant expression.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..18
```

```
FT                   /label= signal_sequence
FT   Protein         19..919
FT                   /note= "mature_protein"
FT   Domain          31..185
FT                   /label= Discoidin_I_like_domain
FT   Cleavage-site   304..307
FT                   /label= endopeptidase_furin
FT                   /note= "putative precursor cleavage site"
FT   Region          48..439
FT                   /label= transmembrane_region
FT   Binding-site    580..590
FT                   /label= ATP_binding_motif
FT   Modified-site   765..766
FT                   /label= autophosphorylation_sites
FT                   /note= "putative"
FT   Modified-site   761
FT                   /label= autophosphorylation_site
FT                   /note= "putative"
FT   Binding-site    807..810
FT                   /label= binding_motif_for_P13_kinase
FT                   /note= "binding motif for phosphatidylinositol 3'
FT                          kinase"
FT   Binding-site    795..795
FT                   /label= potential_substrate_binding_site
FT   Region          26..42
FT                   /note= "antibody recognition sequence NTalpha"
FT   Region          309..321
FT                   /note= "antibody recognition sequence NTbeta"
FT   Region          865..882
FT                   /note= "antibody recognition sequence CTbeta"
XX
PN   US5677144-A.
XX
PD   14-OCT-1997.
XX
PF   08-NOV-1994;   94US-0336343.
XX
PR   16-NOV-1993;   93US-0153397.
XX
PA   (ALVE/) ALVES F H E.
PA   (ULLR/) ULLRICH A.
XX
PI   Alves FHE;  Ullrich A;
XX
DR   WPI; 1997-511869/47.
XX
PT   Truncated receptor tyrosine kinase CCK-2 - and nucleic acid coding
PT   for it, useful for cancer diagnosis
XX
PS   Disclosure; Page -; 70pp; English.
XX
CC   The present sequence represents a splice variant of a mammary
CC   carcinoma kinase (MCK-10). This kinase belongs to a novel family
CC   of receptor tyrosine kinases, and expression is associated with
CC   proliferative diseases such as cancer. The MCK-10 receptor tyrosine
CC   kinase has extensive sequence similarity to the insulin receptor family.
CC   The MCK-10 gene was isolated by PCR using 2 degenerate oligonucleotide
CC   primer pools, using a template cDNA synthesised by reverse transcription
CC   of poly-A RNA from the human mammary carcinoma cell line MCF7. The
CC   amplified PCR product was used to screen human foetal brain and
CC   placental libraries, from which the present splice variant was isolated.
CC   This splice variant does not possess amino acids 505-541 of MCK-10
CC   (AAW34672). The sequence represented by amino acids 548-558 may be
CC   important, as deletion of this motif in the activin receptor
CC   serine/threonine kinase results in reduced ligand binding affinity.
CC   MCK-10 is expressed in brain tissue, and the protein shares homology with
CC   the tyrosine kinase neurotropin receptor. Modulation of MCK-10 activity
CC   therefore may be used for treatment of neurological disorders. MCK-10 is
CC   also expressed in a variety of cancer cell lines and tumour tissue. The
CC   nucleotide sequence of MCK-10, or parts of it, can be used for diagnostic
CC   purposes to detect aberrant expression of MCK-10 genes. Inhibitors of
CC   MCK-10 (or splice variants) receptor activity may have therapeutic value
CC   in the treatment of diseases such as cancer.
CC   note: the present sequence does not appear in the specification, but was
CC   created using information provided.
XX
SQ   Sequence   882 AA;


  Query Match            95.3%;  Score 4697.5;  DB 18;  Length 882;
  Best Local Similarity  96.0%;  Pred. No. 0;
  Matches  882;  Conservative    0;  Mismatches    0;  Indels   37;  Gaps    1;

Qy       1 MGPEALSSLLLLLLVASGDADMKGHFDPAKCRYALGMQDRTIPDSDISASSSWSDSTAAR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mgpealssllllllvasgdadmkghfdpakcryalgmqdrtipdsdisassswsdstaar 60

Qy      61 HSRLESSDGDGAWCPAGSVFPKEEEYLQVDLQRLHLVALVGTQGRHAGGLGKEFSRSYRL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 hsrlessdgdgawcpagsvfpkeeeylqvdlqrlhlvalvgtqgrhagglgkefsrsyrl 120

Qy     121 RYSRDGRRWMGWKDRWGQEVISGNEDPEGVVLKDLGPPMVARLVRFYPRADRVMSVCLRV 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 rysrdgrrwmgwkdrwgqevisgnedpegvvlkdlgppmvarlvrfypradrvmsvclrv 180

Qy     181 ELYGCLWRDGLLSYTAPVGQTMYLSEAVYLNDSTYDGHTVGGLQYGGLGQLADGVVGLDD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 elygclwrdgllsytapvgqtmylseavylndstydghtvgglqygglgqladgvvgldd 240

Qy     241 FRKSQELRVWPGYDYVGWSNHSFSSGYVEMEFEFDRLRAFQAMQVHCNNMHTLGARLPGG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 frksqelrvwpgydyvgwsnhsfssgyvemefefdrlrafqamqvhcnnmhtlgarlpgg 300

Qy     301 VECRFRRGPAMAWEGEPMRHNLGGNLGDPRARAVSVPLGGRVARFLQCRFLFAGPWLLFS 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 vecrfrrgpamawegepmrhnlggnlgdpraravsvplggrvarflqcrflfagpwllfs 360

Qy     361 EISFISDVVNNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTAILI 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 eisfisdvvnnsspalggtfppapwwppgppptnfsslelеprgqqpvakaegsptaili 420

Qy     421 GCLVAIILLLLLIIALMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTILINNRPGPRE 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 gclvaiillllliialmlwrlhwrrllskaerrvleeeltvhlsvpgdtilinnrpgpre 480

Qy     481 PPPYQEPRPRGNPPHSAPCVPNGSALLLSNPAYRLLLATYARPPRGPGPPTPAWAKPTNT 540
           ||||||||||||||||||||||
Db     481 pppyqeprprgnpphsapcvpngs---------------------------------- 504

Qy     541 QAYSGDYMEPEKPGAPLLPPPPQNSVPHYAEADIVTLQGVTGGNTYAVPALPPGAVGDGP 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     505 -aysgdymepekpgapllppppqnsvphyaeadivtlqgvtggntyavpalppgavgdgp 563

Qy     601 PRVDFPRSRLRFKEKLGEGQFGEVHLCEVDSPQDLVSLDFPLNVRKGHPLLVAVKILRPD 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     564 prvdfprsrlrfkeklgegqfgevhlcevdspqdlvsldfplnvrkghpllvavkilrpd 623

Qy     661 ATKNASFSLFSRNDFLKEVKIMSRLKDPNIIRLLGVCVQDDPLCMITDYMENGDLNQFLS 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     624 atknasfslfsrndflkevkimsrlkdpniirllgvcvqddplcmitdymengdlnqfls 683

Qy     721 AHQLEDKAAEGAPGDGQAAQGPTISYPMLLHVAAQIASGMRYLATLNFVHRDLATRNCLV 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     684 ahqledkaaegapgdgqaaqgptisypmllhvaaqiasgmrylatlnfvhrdlatrnclv 743

Qy     781 GENFTIKIADFGMSRNLYAGDYYRVQGRAVLPIRWMAWECILMGKFTTASDVWAFGVTLW 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     744 genftikiadfgmsrnlyagdyyrvqgravlpirwmawecilmgkfttasdvwafgvtlw 803

Qy     841 EVLMLCRAQPFGQLTDEQVIENAGEFFRDQGRQVYLSRPPACPQGLYELMLRCWSRESEQ 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     804 evlmlcraqpfgqltdeqvienageffrdqgrqvylsrppacpqglyelmlrcwsreseq 863

Qy     901 RPPFSQLHRFLAEDALNTV 919
           ||||||||||||||||||
Db     864 rppfsqlhrflaedalntv 882
```

```
RESULT   6
AAW34675
ID   AAW34675 standard; Protein; 876 AA.
XX
AC   AAW34675;
XX
DT   17-FEB-1998  (first entry)
XX
DE   Human mammary carcinoma kinase 10 (MCK-10) spice variant 3.
XX
KW   Mammary carcinoma kinase; MCK-10; receptor tyrosine kinase;
KW   proliferative disease; cancer; insulin receptor family;
KW   tyrosine kinase neurotropin receptor; MCK-10 activity;
KW   neurological disorder; aberrant expression.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..18
FT                   /label= signal_sequence
FT   Protein         19..876
FT                   /note= "mature_protein"
FT   Domain          31..185
FT                   /label= Discoidin_I_like_domain
FT   Cleavage-site   304..307
FT                   /label= endopeptidase_furin
FT                   /note= "putative precursor cleavage site"
FT   Region          48..439
FT                   /label= transmembrane_region
FT   Binding-site    580..590
FT                   /label= ATP_binding_motif
FT   Modified-site   760..761
FT                   /label= autophosphorylation_sites
FT                   /note= "putative"
FT   Modified-site   756..756
FT                   /label= autophosphorylation_site
FT                   /note= "putative"
FT   Binding-site    802..805
FT                   /label= binding_motif_for_P13_kinase
FT                   /note= "binding motif for phosphatidylinositol 3'
FT                        kinase"
FT   Binding-site    790
FT                   /label= potential_substrate_binding_site
FT   Region          26..42
FT                   /note= "antibody recognition sequence NTalpha"
FT   Region          309..321
FT                   /note= "antibody recognition sequence NTbeta"
FT   Region          860..877
FT                   /note= "antibody recognition sequence CTbeta"
XX
PN   US5677144-A.
XX
PD   14-OCT-1997.
XX
PF   08-NOV-1994;   94US-0336343.
XX
PR   16-NOV-1993;   93US-0153397.
XX
PA   (ALVE/) ALVES F H E.
PA   (ULLR/) ULLRICH A.
XX
PI   Alves FHE,  Ullrich A;
XX
DR   WPI; 1997-511869/47.
XX
PT   Truncated receptor tyrosine kinase CCK-2 - and nucleic acid coding
PT   for it, useful for cancer diagnosis
XX
PS   Disclosure; Page -; 70pp; English.
XX
CC   The present sequence represents a splice variant of a mammary
CC   carcinoma kinase (MCK-10). This kinase belongs to a novel family
CC   of receptor tyrosine kinases, and expression is associated with
CC   proliferative diseases such as cancer. The MCK-10 receptor tyrosine
CC   kinase has extensive sequence similarity to the insulin receptor family.
CC   The MCK-10 gene was isolated by PCR using 2 degenerate oligonucleotide
CC   primer pools, using a template cDNA synthesised by reverse transcription
CC   of poly-A RNA from the human mammary carcinoma cell line MCF7. The
CC   amplified PCR product was used to screen human foetal brain and
CC   placental libraries, from which the present splice variant was isolated.
CC   This splice variant does not possess amino acids 505-541 or 666-671 of
CC   MCK-10 (AAW34672). The sequence represented by amino acids 548-558 may
CC   be important, as deletion of this motif in the activin receptor
CC   serine/threonine kinase results in reduced ligand binding affinity.
CC   MCK-10 is expressed in brain tissue, and the protein shares homology
CC   with the tyrosine kinase neurotropin receptor. Modulation of MCK-10
CC   activity therefore may be used for treatment of neurological disorders.
CC   MCK-10 is also expressed in a variety of cancer cell lines and tumour
CC   tissue. The nucleotide sequence of MCK-10, or parts of it, can be used
CC   for diagnostic purposes to detect aberrant expression of MCK-10 genes.
CC   Inhibitors of MCK-10 (or splice variants) receptor activity may have
CC   therapeutic value in the treatment of diseases such as cancer.
CC   note: the present sequence does not appear in the specification, but was
CC   created using information provided.
XX
SQ   Sequence   876 AA;


  Query Match             94.5%;  Score 4656.5;  DB 18;  Length 876;
  Best Local Similarity   95.3%;  Pred. No. 0;
  Matches  876;  Conservative    0;  Mismatches    0;  Indels   43;  Gaps    2;

Qy       1 MGPEALSSLLLLLLVASGDADMKGHFDPAKCRYALGMQDRTIPDSDISASSSWSDSTAAR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mgpealssllllllvasgdadmkghfdpakcryalgmqdrtipdsdisassswsdstaar 60

Qy      61 HSRLESSDGDGAWCPAGSVFPKEEEYLQVDLQRLHLVALVGTQGRHAGGLGKEFSRSYRL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 hsrlessdgdgawcpagsvfpkeeeylqvdlqrlhlvalvgtqgrhagglgkefsrsyrl 120

Qy     121 RYSRDGRRWMGWKDRWGQEVISGNEDPEGVVLKDLGPPMVARLVRFYPRADRVMSVCLRV 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 rysrdgrrwmgwkdrwgqevisgnedpegvvlkdlgppmvarlvrfypradrvmsvclrv 180

Qy     181 ELYGCLWRDGLLSYTAPVGQTMYLSEAVYLNDSTYDGHTVGGLQYGGLGQLADGVVGLDD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 elygclwrdgllsytapvgqtmylseavylndstydghtvgglqygglgqladgvvgldd 240

Qy     241 FRKSQELRVWPGYDYVGWSNHSFSSGYVEMEFEFDRLRAFQAMQVHCNNMHTLGARLPGG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 frksqelrvwpgydyvgwsnhsfssgyvemefefdrlrafqamqvhcnnmhtlgarlpgg 300

Qy     301 VECRFRRGPAMAWEGEPMRHNLGGNLGDPRARAVSVPLGGRVARFLQCRFLFAGPWLLFS 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 vecrfrrgpamawegepmrhnlggnlgdpraravsvplggrvarflqcrflfagpwllfs 360

Qy     361 EISFISDVVNNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTAILI 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 eisfisdvvnnsspalggtfppapwwppgppptnfsslelеprgqqpvakaegsptaili 420

Qy     421 GCLVAIILLLLLIIALMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTILINNRPGPRE 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 gclvaiilllllliialmlwrlhwrrllskaerrvleeeltvhlsvpgdtilinnrpgpre 480

Qy     481 PPPYQEPRPRGNPPHSAPCVPNGSALLLSNPAYRLLLATYARPPRGPGPPTPAWAKPTNT 540
           ||||||||||||||||||||||||
Db     481 pppyqeprprgnpphsapcvpngs---------------------------------- 504

Qy     541 QAYSGDYMEPEKPGAPLLPPPPQNSVPHYAEADIVTLQGVTGGNTYAVPALPPGAVGDGP 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     505 -aysgdymepekpgapllppppqnsvphyaeadivtlqgvtggntyavpalppgavgdgp 563

Qy     601 PRVDFPRSRLRFKEKLGEGQFGEVHLCEVDSPQDLVSLDFPLNVRKGHPLLVAVKILRPD 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    564 prvdfprsrlrfkeklgegqfgevhlcevdspqdlvsldfplnvrkghpllvavkilrpd 623

Qy    661 ATKNASFSLFSRNDFLKEVKIMSRLKDPNIIRLLGVCVQDDPLCMITDYMENGDLNQFLS 720
          |||||      ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    624 atkna------rndflkevkimsrlkdpniirllgvcvqddplcmitdymengdlnqfls 677

Qy    721 AHQLEDKAAEGAPGDGQAAQGPTISYPMLLHVAAQIASGMRYLATLNFVHRDLATRNCLV 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    678 ahqledkaaegapgdgqaaqgptisypmllhvaaqiasgmrylatlnfvhrdlatrnclv 737

Qy    781 GENFTIKIADFGMSRNLYAGDYYRVQGRAVLPIRWMAWECILMGKFTTASDVWAFGVTLW 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    738 genftikiadfgmsrnlyagdyyrvqgravlpirwmawecilmgkfttasdvwafgvtlw 797

Qy    841 EVLMLCRAQPFGQLTDEQVIENAGEFFRDQGRQVYLSRPPACPQGLYELMLRCWSRESEQ 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    798 evlmlcraqpfgqltdeqvienageffrdqgrqvylsrppacpqglyelmlrcwsreseq 857

Qy    901 RPPFSQLHRFLAEDALNTV 919
          ||||||||||||||||||
Db    858 rppfsqlhrflaedalntv 876
```

```
RESULT   7
AAB54286
ID   AAB54286 standard; Protein; 624 AA.
XX
AC   AAB54286;
XX
DT   09-MAR-2001  (first entry)
XX
DE   Human pancreatic cancer antigen protein sequence SEQ ID NO:738.
XX
KW   Human; pancreas; pancreatic cancer; pancreatic cancer antigen;
KW   detection; diagnosis; identification; cytostatic; neuroprotective;
KW   nootropic; immunomodulatory; relaxant; contraceptive; gynaecological;
KW   antiinflammatory; cardiant; gene therapy; chromosome mapping;
KW   linkage analysis; tissue identification; tissue typing; forensic;
KW   neural; immune system; muscular; reproductive; gastrointestinal;
KW   pulmonary; cardiovascular; renal; proliferative.
XX
OS   Homo sapiens.
XX
PN   WO200055320-A1.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US05989.
XX
PR   12-MAR-1999;   99US-0124270.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2000-579444/54.
DR   N-PSDB; AAC99051.
XX
PT   New nucleic acid that is a pancreatic cancer antigen for preventing,
PT   treating, or ameliorating a medical condition, particular pancreatic
PT   cancer, or for use in assays for diagnosing a pathological condition -
XX
PS   Claim 11; Page 1180-1182; 1379pp; English.
XX
CC   AAC98773 to AAC99231 encode the human pancreatic cancer associated
CC   proteins, called pancreatic cancer antigens, given in AAB54008 to
CC   AAB54466. The human pancreatic cancer antigens have cytostatic,
CC   neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive,
CC   gynaecological, cardiant and antiinflammatory activities, and can be used
CC   in gene therapy. The polynucleotide and proteins can be used for
CC   preventing, treating, or ameliorating a medical condition or in assays
CC   for diagnosing a pathological condition or a susceptibility to one in a
CC   subject. Binding partners to the proteins and the activity of the
CC   proteins can be identified. The pancreatic cancer antigens can be used to
CC   detect, treat or prevent pancreatic disorders, especially cancer.
CC   Agonists and antagonists to the antigens can be screened for. The
CC   pancreatic cancer antigen polynucleotides can be used to design nucleic
CC   acid hybridisation probes that can be used in chromosome mapping, linkage
CC   analysis, tissue identification and/or typing and a variety of forensic
CC   and diagnostic methods. The proteins can be used to generate antibodies
CC   which are used to purify, detect and target the polypeptides, including
CC   both in vivo and in vitro diagnostic and therapeutic methods. The
CC   proteins can be used to treat or prevent neural, immune system, muscular,
CC   reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
CC   proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
CC   sequences used in the exemplification of the present invention.
XX
SQ   Sequence   624 AA;
```

```
  Query Match          66.9%;  Score 3298;  DB 21;  Length 624;
  Best Local Similarity   98.7%;  Pred. No. 7.7e-245;
  Matches  616;  Conservative    0;  Mismatches    2;  Indels    6;  Gaps    1;

Qy    261 HSFSSGYVEMEFEFDRLRAFQAMQVHCNNMHTLGARLPGGVECRFRRGPAMAWEGEPMRH 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3 hsfssgyvemefefdrlrafqamqvhcnnmhtlgarlpggvecrfrrgpamawegepmrh 62

Qy    321 NLGGNLGDPRARAVSVPLGGRVARFLQCRFLFAGPWLLFSEISFISDVVNNSSPALGGTF 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     63 nlggnlgdpraravsvplggrvarflqcrflfagpwllfseisfisdvvnnsspalggtf 122

Qy    381 PPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTAILIGCLVAIILLLLLIIALMLWR 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 ppapwwppgppptnfsslelеprgqqpvakaegsptailigclvaiillllliialmlwr 182

Qy    441 LHWRRLLSKAERRVLEEELTVHLSVPGDTILINNRPGPREPPPYQEPRPRGNPPHSAPCV 500
          ||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    183 lhwrrxlskxerrvleeeltvhlsvpgdtilinnrpgprepppyqeprprgnpphsapcv 242

Qy    501 PNGSALLLSNPAYRLLLATYARPPRGPGPPTPAWAKPTNTQAYSGDYMEPEKPGAPLLPP 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    243 pngsalllsnpayrlllatyarpprgpgpptpawakptntqaysgdymepekpgapllpp 302

Qy    561 PPQNSVPHYAEADIVTLQGVTGGNTYAVPALPPGAVGDGPPRVDFPRSRLRFKEKLGEGQ 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    303 ppqnsvphyaeadivtlqgvtggntyavpalppgavgdgpprvdfprsrlrfkeklgegq 362

Qy    621 FGEVHLCEVDSPQDLVSLDFPLNVRKGHPLLVAVKILRPDATKNASFSLFSRNDFLKEVK 680
          |||||||||||||||||||||||||||||||||||||||||||||      |||||||||
Db    363 fgevhlcevdspqdlvsldfplnvrkghpllvavkilrpdatkna------rndflkevk 416

Qy    681 IMSRLKDPNIIRLLGVCVQDDPLCMITDYMENGDLNQFLSAHQLEDKAAEGAPGDGQAAQ 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    417 imsrlkdpniirllgvcvqddplcmitdymengdlnqflsahqledkaaegapgdgqaaq 476

Qy    741 GPTISYPMLLHVAAQIASGMRYLATLNFVHRDLATRNCLVGENFTIKIADFGMSRNLYAG 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    477 gptisypmllhvaaqiasgmrylatlnfvhrdlatrnclvgenftikiadfgmsrnlyag 536

Qy    801 DYYRVQGRAVLPIRWMAWECILMGKFTTASDVWAFGVTLWEVLMLCRAQPFGQLTDEQVI 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    537 dyyrvqgravlpirwmawecilmgkfttasdvwafgvtlwevlmlcraqpfgqltdeqvi 596

Qy    861 ENAGEFFRDQGRQVYLSRPPACPQ 884
          ||||||||||||||||||||||||
Db    597 enageffrdqgrqvylsrppacpq 620
```

```
RESULT   8
AAG73767
ID   AAG73767 standard; Protein; 624 AA.
XX
AC   AAG73767;
XX
DT   03-SEP-2001  (first entry)
```

```
XX
DE   Human colon cancer antigen protein SEQ ID NO:4531.
XX
KW   Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW   colorectal carcinoma; chromosome 6.
XX
OS   Homo sapiens.
XX
PN   WO200122920-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-US26524.
XX
PR   29-SEP-1999;   99US-0157137.
PR   03-NOV-1999;   99US-0163280.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Barash SC,  Birse CE,  Rosen CA;
XX
DR   WPI; 2001-235357/24.
DR   N-PSDB; AAH33198.
XX
PT   Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT   useful for preventing, diagnosing and/or treating colorectal cancers -
XX
PS   Claim 11; Page 6327-6329; 9803pp; English.
XX
CC   AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC   cancer-associated nucleic acid molecules (N) and proteins (P), where
CC   the proteins are collectively known as colon cancer antigens. The colon
CC   cancer antigens have cytostatic activity and can be used in gene
CC   therapy and vaccine production. N and P may be used in the prevention,
CC   diagnosis and treatment of diseases associated with inappropriate P
CC   expression. For example, N and P may be used to treat disorders
CC   associated with decreased expression by rectifying mutations or deletions
CC   in a patient's genome that affect the activity of P by expressing
CC   inactive proteins or to supplement the patients own production of P.
CC   Additionally, N may be used to produce the colon cancer-associated Ps,
CC   by inserting the nucleic acids into a host cell and culturing the cell
CC   to express the proteins. N and P can be used in the prevention, diagnosis
CC   and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC   and AAB77789 represent sequences used in the exemplification of the
CC   present invention.
CC   N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC   missing at time of publication, meaning no sequences are present for
CC   SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ   Sequence   624 AA;


  Query Match            66.9%;  Score 3298;  DB 22;  Length 624;
  Best Local Similarity  98.7%;  Pred. No. 7.7e-245;
  Matches  616;  Conservative    0;  Mismatches    2;  Indels    6;  Gaps    1;

Qy    261 HSFSSGYVEMEFEFDRLRAFQAMQVHCNNMHTLGARLPGGVECRFRRGPAMAWEGEPMRH 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3 hsfssgyvemefefdrlrafqamqvhcnnmhtlgarlpggvecrfrrgpamawegepmrh 62

Qy    321 NLGGNLGDPRARAVSVPLGGRVARFLQCRFLFAGPWLLFSEISFISDVVNNSSPALGGTF 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     63 nlggnlgdpraravsvplggrvarflqcrflfagpwllfseisfisdvvnnsspalggtf 122

Qy    381 PPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTAILIGCLVAIILLLLLIIALMLWR 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 ppapwwppgppptnfssleleprgqqpvakaegsptailigclvaiilllllliialmlwr 182

Qy    441 LHWRRLLSKAERRVLEEELTVHLSVPGDTILINNRPGPREPPPYQEPRPRGNPPHSAPCV 500
          ||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    183 lhwrrxlskxerrvleeeltvhlsvpgdtilinnrpgprepppyqeprprgnpphsapcv 242

Qy    501 PNGSALLLSNPAYRLLLATYARPPRGPGPPTPAWAKPTNTQAYSGDYMEPEKPGAPLLPP 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    243 pngsalllsnpayrlllatyarpprgpgpptpawakptntqaysgdymepekpgapllpp 302

Qy    561 PPQNSVPHYAEADIVTLQGVTGGNTYAVPALPPGAVGDGPPRVDFPRSRLRFKEKLGEGQ 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    303 ppqnsvphyaeadivtlqgvtggntyavpalppgavgdgpprvdfprsrlrfkeklgegq 362

Qy    621 FGEVHLCEVDSPQDLVSLDFPLNVRKGHPLLVAVKILRPDATKNASFSLFSRNDFLKEVK 680
          ||||||||||||||||||||||||||||||||||||||||||||      |||||||||
Db    363 fgevhlcevdspqdlvsldfplnvrkghpllvavkilrpdatkna------rndflkevk 416

Qy    681 IMSRLKDPNIIRLLGVCVQDDPLCMITDYMENGDLNQFLSAHQLEDKAAEGAPGDGQAAQ 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    417 imsrlkdpniirllgvcvqddplcmitdymengdlnqflsahqledkaaegapgdgqaaq 476

Qy    741 GPTISYPMLLHVAAQIASGMRYLATLNFVHRDLATRNCLVGENFTIKIADFGMSRNLYAG 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    477 gptisypmllhvaaqiasgmrylatlnfvhrdlatrnclvgenftikiadfgmsrnlyag 536

Qy    801 DYYRVQGRAVLPIRWMAWECILMGKFTTASDVWAFGVTLWEVLMLCRAQPFGQLTDEQVI 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    537 dyyrvqgravlpirwmawecilmgkfttasdvwafgvtlwevlmlcraqpfgqltdeqvi 596

Qy    861 ENAGEFFRDQGRQVYLSRPPACPQ 884
          |||||||||||||||||||||||
Db    597 enageffrdqgrqvylsrppacpq 620


RESULT   9
AAW34674
ID   AAW34674 standard; Protein; 563 AA.
XX
AC   AAW34674;
XX
DT   17-FEB-1998  (first entry)
XX
DE   Human mammary carcinoma kinase 10 (MCK-10) spice variant 2.
XX
KW   Mammary carcinoma kinase; MCK-10; receptor tyrosine kinase;
KW   proliferative disease; cancer; insulin receptor family;
KW   tyrosine kinase neurotropin receptor; MCK-10 activity;
KW   neurological disorder; aberrant expression.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide          1..18
FT                    /label= signal_sequence
FT   Protein          19..919
FT                    /note= "mature_protein"
FT   Domain           31..185
FT                    /label= Discoidin_I_like_domain
FT   Cleavage-site    304..307
FT                    /label= endopeptidase_furin
FT                    /note= "putative precursor cleavage site"
FT   Region           48..439
FT                    /label= transmembrane_region
FT   Binding-site     617..627
FT                    /label= ATP_binding_motif
FT   Modified-site    797..798
FT                    /label= autophosphorylation_sites
FT                    /note= "putative"
FT   Modified-site    793
FT                    /label= autophosphorylation_site
FT                    /note= "putative"
FT   Binding-site     839..842
FT                    /label= binding_motif_for_P13_kinase
FT                    /note= "binding motif for phosphatidylinositol 3'
FT                          kinase"
FT   Binding-site     827..827
FT                    /label= potential_substrate_binding_site
FT   Binding-site     506..509
FT                    /label= putative_receptor_binding_site_for_SHC
```

```
FT                  /note= "SHC is an oncogenic SH2 domain containing
FT                        molecule"
FT   Binding-site   510..513
FT                  /label= GTPase_activity_protein_binding_site
FT                  /note= "putative"
FT   Region         26..42
FT                  /note= "antibody recognition sequence NTalpha"
FT   Region         309..321
FT                  /note= "antibody recognition sequence NTbeta"
FT   Region         897..913
FT                  /note= "antibody recognition sequence CTbeta"
XX
PN   US5677144-A.
XX
PD   14-OCT-1997.
XX
PF   08-NOV-1994;   94US-0336343.
XX
PR   16-NOV-1993;   93US-0153397.
XX
PA   (ALVE/) ALVES F H E.
PA   (ULLR/) ULLRICH A.
XX
PI   Alves FHE,  Ullrich A;
XX
DR   WPI; 1997-511869/47.
XX
PT   Truncated receptor tyrosine kinase CCK-2 - and nucleic acid coding
PT   for it, useful for cancer diagnosis
XX
PS   Disclosure; Page -; 70pp; English.
XX
CC   The present sequence represents a splice variant of a mammary
CC   carcinoma kinase (MCK-10). This kinase belongs to a novel family
CC   of receptor tyrosine kinases, and expression is associated with
CC   proliferative diseases such as cancer. The MCK-10 receptor tyrosine
CC   kinase has extensive sequence similarity to the insulin receptor family.
CC   The MCK-10 gene was isolated by PCR using 2 degenerate oligonucleotide
CC   primer pools, using a template cDNA synthesised by reverse transcription
CC   of poly-A RNA from the human mammary carcinoma cell line MCF7. The
CC   amplified PCR product was used to screen human foetal brain and
CC   placental libraries, from which the present splice variant was isolated.
CC   This splice variant does not possess amino acids 666-671 of MCK-10
CC   (AAW34672). The sequence represented by amino acids 585-595 may be
CC   important, as deletion of this motif in the activin receptor
CC   serine/threonine kinase results in reduced ligand binding affinity.
CC   MCK-10 is expressed in brain tissue, and the protein shares homology with
CC   the tyrosine kinase neurotropin receptor. Modulation of MCK-10 activity
CC   therefore may be used for treatment of neurological disorders. MCK-10 is
CC   also expressed in a variety of cancer cell lines and tumour tissue. The
CC   nucleotide sequence of MCK-10, or parts of it, can be used for diagnostic
CC   purposes to detect aberrant expression of MCK-10 genes. Inhibitors of
CC   MCK-10 (or splice variants) receptor activity may have therapeutic value
CC   in the treatment of diseases such as cancer.
CC   note: the present sequence does not appear in the specification, but was
CC   created using information provided.
XX
SQ   Sequence   563 AA;


  Query Match             60.9%;  Score 3003;  DB 18;  Length 563;
  Best Local Similarity   98.9%;  Pred. No. 3.1e-222;
  Matches  563;  Conservative    0;  Mismatches    0;  Indels    6;  Gaps    1;

Qy     351 LFAGPWLLFSEISFISDVVNNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAK 410
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 lfagpwllfseisfisdvvnnsspalggtfppapwwppgppptnfsslleleprgqqpvak 60

Qy     411 AEGSPTAILIGCLVAIILLLLLIIALMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTI 470
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 aegsptailigclvaiillllliialmlwrlhwrrllskaerrvleeeltvhlsvpgdti 120

Qy     471 LINNRPGPREPPPYQEPRPRGNPPHSAPCVPNGSALLLSNPAYRLLLATYARPPRGPGPP 530
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 linnrpgpreppppyqeprprgnpphsapcvpngsalllsnpayrlllatyarpprgpgpp 180

Qy     531 TPAWAKPTNTQAYSGDYMEPEKPGAPLLPPPPQNSVPHYAEADIVTLQGVTGGNTYAVPA 590
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 tpawakptntqaysgdymepekpgapllppppqnsvphyaeadivtlqgvtggntyavpa 240

Qy     591 LPPGAVGDGPPRVDFPRSRLRFKEKLGEGQFGEVHLCEVDSPQDLVSLDFPLNVRKGHPL 650
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 lppgavgdgpprvdfprsrlrfkeklgegqfgevhlcevdspqdlvsldfplnvrkghpl 300

Qy     651 LVAVKILRPDATKNASFSLFSRNDFLKEVKIMSRLKDPNIIRLLGVCVQDDPLCMITDYM 710
           ||||||||||||||      ||||||||||||||||||||||||||||||||||||||||
Db     301 lvavkilrpdatkna------rndflkevkimsrlkdpniirllgvcvqddplcmitdym 354

Qy     711 ENGDLNQFLSAHQLEDKAAEGAPGDGQAAQGPTISYPMLLHVAAQIASGMRYLATLNFVH 770
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     355 engdlnqflsahqledkaaegapgdgqaaqgptisypmllhvaaqiasgmrylatlnfvh 414

Qy     771 RDLATRNCLVGENFTIKIADFGMSRNLYAGDYYRVQGRAVLPIRWMAWECILMGKFTTAS 830
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     415 rdlatrnclvgenftikiadfgmsrnlyagdyyrvqgravlpirwmawecilmgkfttas 474

Qy     831 DVWAFGVTLWEVLMLCRAQPFGQLTDEQVIENAGEFFRDQGRQVYLSRPPACPQGLYELM 890
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     475 dvwafgvtlwevlmlcraqpfgqltdeqvienageffrdqgrqvylsrppacpqglyelm 534

Qy     891 LRCWSRESEQRPPFSQLHRFLAEDALNTV 919
           |||||||||||||||||||||||||||||
Db     535 lrcwsreseqrppfsqlhrflaedalntv 563
```

```
RESULT  10
AAR75503
ID   AAR75503 standard; Protein; 855 AA.
XX
AC   AAR75503;
XX
DT   26-NOV-1995  (first entry)
XX
DE   Human colonic adenocarcinoma kinase 2 (CCK-2).
XX
KW   Mammary carcinoma kinase 10; MCK-10; transmembrane receptor; CCK-2;
KW   receptor tyrosine kinase; colonic adenocarcinoma kinase 2; cancer.
XX
OS   Homo sapiens.
XX
PN   WO9514088-A.
XX
PD   26-MAY-1995.
XX
PF   16-NOV-1994;   94WO-EP03797.
XX
PR   16-NOV-1993;   93US-0153397.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Alves FHE,  Ullrich A;
XX
DR   WPI; 1995-224054/29.
DR   N-PSDB; AAQ92521.
XX
PT   New nucleic acid encoding MCK-10 receptor tyrosine kinase - and
PT   derived vectors, transformed cells, proteins and antibodies useful
PT   for diagnosis and treatment of proliferative disease, esp. cancer,
PT   and for screening modulators
XX
PS   Disclosure; Page 57-60; 115pp; English.
XX
CC   A member of the mammary carcinomal kinase 10 (MCK-10) receptor
CC   tyrosine kinase family was identified using a PCR (with two degenerate
CC   oligo primer pools based on conserved sequences of the kinase domain of
CC   receptor tyrosine kinases) and cDNA prepd. from colonic
```

```
CC   adenocarcinoma RNA. The nt sequence of the novel receptor,
CC   designated CCK-2, is given in AAQ92521 and the deduced AA sequence in
CC   AAR75503. Analysis of the CCK-2 nt and AA sequence indicated
CC   significant homology with MCK-10 throughout the extracellular,
CC   transmembrane and intracellular regions. The regions of homology
CC   extend into the N-terminus consensus sequence for the discoidin I
CC   like family of proteins.
XX
SQ   Sequence   855 AA;


  Query Match             48.8%;  Score 2404;  DB 16;  Length 855;
  Best Local Similarity   51.8%;  Pred. No. 5.7e-176;
  Matches  482;  Conservative  118;  Mismatches  227;  Indels  104;  Gaps   16;

Qy       3 PEALSSLLLLLLVASGDADMKGHFDPAKCRYALGMQDRTIPDSDISASSSWSDSTAARHS 62
Db       5 prmllvlfllpils---sakaqvnpaicryplgmsggqipdeditassqwsestaakyg 61

Qy      63 RLESSDGDGAWCPAGSVFPKE-EEYLQVDLQRLHLVALVGTQGRHAGGLGKEFSRSYRLR 121
Db      62 rldseegdgawcpeipvepddlkeflqidlhtlhfitlvgtqgrhagghgiefapmykin 121

Qy     122 YSRDGRRWMGWKDRWGQEVISGNEDPEGVVLKDLGPPMVARLVRFYPRADRVMSVCLRVE 181
Db     122 ysrdgtrwiswrnrhgkqvldgnsnpydiflkdleppivarfvrfipvtdhsmnvcmrve 181

Qy     182 LYGCLWRDGLLSYTAPVGQTMYL--SEAVYLNDSTYDGHTVGGLQYGGLGQLADGVVGLD 239
Db     182 lygcvwldglvsynapagqqfvlpggsiiylndsvydg-avgysmteglgqltdgvsgld 240

Qy     240 DFRKSQELRVWPGYDYVGWSNHSFSSGYVEMEFEFDRLRAFQAMQVHCNNMHTLGARLPG 299
Db     241 dftqtheyhvwpgydyvgwrnesatngyieimfefdrirnfttmkvhcnnmfakgvkifk 300

Qy     300 GVECRFRRGPAMAWEGEPMRHNLGGNLGDPRARAVSVPLGGRVARFLQCRFLFAGPWLLF 359
Db     301 evqcyf-rseasewepnaisfplvlddvnpsarfvtvplhhrmasaikcqyhfadtwmmf 359

Qy     360 SEISFISD-VVNNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTAI 418
Db     360 seitfqsdaamynnseal----ptsp--------------mapttydpmlkvddsntri 400

Qy     419 LIGCLVAIILLLLLIIALMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTILINNR--P 476
Db     401 ligclvaiifillaiiviilwrqfwqkmlekasrrmlddemtvslslpsdssmfnnnrss 460

Qy     477 GPREP-------------PPYQEPRPRGNPPHSAPCVPNGSALLLSNPAYRLLLATYARP 523
Db     461 spseqgsnstydrifplrpdyqep---------------srlirklpef---------- 494

Qy     524 PRGPGPPTPAWAKPTNTQAYSGDYMEPEKPGAPLLPPPPQNSVPHYAEADIVTLQGVTGG 583
Db     495 ------------apgeeesgcsgvvkpvqpsgp-------egvphyaeadivnlqgvtgg 535

Qy     584 NTYAVPALPPGAVGDGPPRV-DFPRSRLRFKEKLGEGQFGEVHLCEVDSPQDLVSLDFPL 642
Db     536 ntysvpavtmdllsgkdvaveefprklltfkeklgegqfgevhlcevegmekfkdkdfal 595

Qy     643 NVRKGHPLLVAVKILRPDATKNASFSLFSRNDFLKEVKIMSRLKDPNIIRLLGVCVQDDP 702
Db     596 dvsanqpvlvavkmlradankna------rndflkeikimsrlkdpniihllsvcitddp 649

Qy     703 LCMITDYMENGDLNQFLSAHQLEDKAAEGAPGDGQAAQGPTISYPMLLHVAAQIASGMRY 762
Db     650 lcmiteymengdlnqflsrhe---------ppnssssdvrtvsytnlkfmatqiasgmky 700

Qy     763 LATLNFVHRDLATRNCLVGENFTIKIADFGMSRNLYAGDYYRVQGRAVLPIRWMAWECIL 822
Db     701 lsslnfvhrdlatrnclvgknytikiadfgmsrnlysgdyyriqgravlpirwmswesil 760

Qy     823 MGKFTTASDVWAFGVTLWEVLMLCRAQPFGQLTDEQVIENAGEFFRDQGRQVYLSRPPAC 882
Db     761 lgkfttasdvwafgvtlwetftfcqeqpysqlsdeqvientgeffrdqgrqtylpqpaic 820

Qy     883 PQGLYELMLRCWSRESEQRPPFSQLHRFLAE 913
Db     821 pdsvyklmlscwrrdtknrpsfqeihllllq 851


RESULT  11
AAR75505
ID   AAR75505 standard; Protein; 855 AA.
XX
AC   AAR75505;
XX
DT   26-NOV-1995  (first entry)
XX
DE   Human colonic adenocarcinoma kinase 2 (CCK-2).
XX
KW   Mammary carcinoma kinase 10; MCK-10; transmembrane receptor; CCK-2;
KW   receptor tyrosine kinase; colonic adenocarcinoma kinase 2.
XX
OS   Homo sapiens.
XX
PN   WO9514089-A.
XX
PD   26-MAY-1995.
XX
PF   16-NOV-1994;   94WO-EP03799.
XX
PR   16-NOV-1993;   93US-0153397.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Alves FHE,  Ullrich A;
XX
DR   WPI; 1995-224055/29.
DR   N-PSDB; AAQ92523.
XX
PT   New nucleic acid encoding CCK-2 receptor tyrosine kinase - and
PT   derived vectors, transformed cells, proteins and antibodies, useful
PT   for diagnosis and treatment of proliferative and nervous system
PT   diseases and for screening modulators
XX
PS   Disclosure; Page 74-77; 115pp; English.
XX
CC   A member of the mammary carcinomal kinase 10 (MCK-10) receptor
CC   tyrosine kinase family was identified using a PCR (with two
CC   degenerate oligo primer pools based on conserved sequences of the
CC   kinase domains of receptor tyrosine kinases) and cDNA prepd. from
CC   colonic adenocarcinoma RNA. The nt sequence of the novel receptor,
CC   designated CCK-2, is given in AAQ92523 and the deduced AA sequence in
CC   AAR75505. Analysis of CCK-2 nt and AA sequences indicated significant
CC   homology with MCK-10 throughout the extracellular, transmembrane
CC   and intracellular regions. The regions of homology extend into the
CC   N-terminus consensus seuence fothe discoidin I like family of
CC   proteins. CCK-2 was predominantly found in all stromal cells
CC   whereas MCK-10 expression was stronglyu confined to neoplastic
CC   cells themselves. Between the two RTKs, the juxtamembrane region
CC   is the region of most extensive sequence divergence.
XX
SQ   Sequence   855 AA;


  Query Match             48.8%;  Score 2404;  DB 16;  Length 855;
  Best Local Similarity   51.8%;  Pred. No. 5.7e-176;
  Matches  482;  Conservative  118;  Mismatches  227;  Indels  104;  Gaps   16;

Qy       3 PEALSSLLLLLLVASGDADMKGHFDPAKCRYALGMQDRTIPDSDISASSSWSDSTAARHS 62
Db       5 prmllvlfllpils---sakaqvnpaicryplgmsggqipdeditassqwsestaakyg 61

Qy      63 RLESSDGDGAWCPAGSVFPKE-EEYLQVDLQRLHLVALVGTQGRHAGGLGKEFSRSYRLR 121
Db      62 rldseegdgawcpeipvepddlkeflqidlhtlhfitlvgtqgrhagghgiefapmykin 121
```

```
Qy    122 YSRDGRRWMGWKDRWGQEVISGNEDPEGVVLKDLGPPMVARLVRFYPRADRVMSVCLRVE 181
          ||||| ||: |::| |::|: || :|  : |||| ||:||| ||| |  |  |:||:|||
Db    122 ysrdgtrwiswrnrhgkqvldgnsnpydiflkdleppivarfvrfipvtdhsmnvcmrve 181

Qy    182 LYGCLWRDGLLSYTAPVGQTMYL--SEAVYLNDSTYDGHTVGGLQYGGLGQLADGVVGLD 239
          ||||:| |||:|| || ||   |     :||||| ||| ||      ||||| ||| |||
Db    182 lygcvwldglvsynapagqqfvlpggsiiylndsvydg-avgysmteglgqltdgvsgld 240

Qy    240 DFRKSQELRVWPGYDYVGWSNHSFSSGYVEMEFEFDRLRAFQAMQVHCNNMHTLGARLPG 299
          || :: |  |||||||||| | | ::||:|: |||||:| |  |:|||||   | ::
Db    241 dftqtheyhvwpgydyvgwrnesatngyieimfefdrirnfttmkvhcnnmfakgvkifk 300

Qy    300 GVECRFRRGPAMAWEGEPMRHNLGGNLGDPRARAVSVPLGGRVARFLQCRFLFAGPWLLF 359
          |:| | |  |  ||   :  |  :  :| || |:|||  |:|  ::|:: ||  |::|
Db    301 evqcyf-rseasewepnaisfpl¥lddvnpsarfvtvplhhrmasaikcqyhfadtwmmf 359

Qy    360 SEISFISD-VVNNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTAI 418
          |||:| ||  : |:| ||    | :|                : |    |: | : | | |
Db    360 seitfqsdaamynnseal----ptsp--------------mapttydpmlkvddsntri 400

Qy    419 LIGCLVAIILLLLLIIALMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTILINNR--P 476
          ||||||||| :|| || ::|||  |:::| || ||:|::|:|| ||:| |: : ||
Db    401 ligclvaiifillaiiviilwrqfwqkmlekasrrmlddemtvslslpsdssmfnnnrss 460

Qy    477 GPREP------------PPYQEPRPRGNPPHSAPCVPNGSALLLSNPAYRLLLATYARP 523
          | |               | ||||               | |:   | :
Db    461 spseqgsnstydrifplrpdyqep---------------srlirklpef---------- 494

Qy    524 PRGPGPPTPAWAKPTNTQAYSGDYMEPEKPGAPLLPPPPQNSVPHYAEADIVTLQGVTGG 583
                |   ::     ::| :|  |         |||||||||| ||||||
Db    495 ------------apgeeesgcsgvvkpvqpsgp-------egvphyaeadivnlqgvtgg 535

Qy    584 NTYAVPALPPGAVGDGPPRV-DFPRSRLRFKEKLGEGQFGEVHLCEVDSPQDLVSLDFPL 642
          |||:|||:    :      | :|||  | |||||||||||||||||:  :     || |
Db    536 ntysvpavtmdllsgkdvaveefprklltfkeklgegqfgevhlcevegmekfkdkdfal 595

Qy    643 NVRKGHPLLVAVKILRPDATKNASFSLFSRNDFLKEVKIMSRLKDPNIIRLLGVCVQDDP 702
          :|    |:|||||:|| || |||      |||||||:|||||||||||| || ||: |||
Db    596 dvsanqpvlvavkmlradankna------rndflkeikimsrlkdpniihllsvcitddp 649

Qy    703 LCMITDYMENGDLNQFLSAHQLEDKAAEGAPGDGQAAQGPTISYPMLLHVAAQIASGMRY 762
          |||||:||||||||||| |:         | :  ::   |:||  |  :| ||||||:|
Db    650 lcmiteymengdlnqflsrhe---------ppnssssdvrtvsytnlkfmatqiasgmky 700

Qy    763 LATLNFVHRDLATRNCLVGENFTIKIADFGMSRNLYAGDYYRVQGRAVLPIRWMAWECIL 822
          |::|||||||||||||||:|:|||||||||||||:|||||:|||||||||||:|| ||
Db    701 lsslnfvhrdlatrnclvgknytikiadfgmsrnlysgdyyriqgravlpirwmswesil 760

Qy    823 MGKFTTASDVWAFGVTLWEVLMLCRAQPFGQLTDEQVIENAGEFFRDQGRQVYLSRPPAC 882
          :|||||||||||||||||    |: ||: ||:|||||| |||||||||| || :|  |
Db    761 lgkfttasdvwafgvtlwetftfcqeqpysqlsdeqvientgeffrdqgrqtylpqpaic 820

Qy    883 PQGLYELMLRCWSRESEQRPPFSQLHRFLAE 913
          |  :|:||| || |::: || | ::|  | :
Db    821 pdsvyklmlscwrrdtknrpsfqeihllllq 851
```

RESULT 12
AAW34671
ID AAW34671 standard; Protein; 855 AA.
XX
AC AAW34671;
XX
DT 16-FEB-1998 (first entry)
XX
DE CCK-2, a human mammary carcinoma kinase 10 MCK-10) family member.
XX
KW Mammary carcinoma kinase; MCK-10; CCK-2; receptor tyrosine kinase;
KW proliferative disease; cancer; MCK-10 activity; aberrant expression.
XX
OS Homo sapiens.
XX

FH Key Location/Qualifiers
FT Modified-site 121
FT /note= "N-glycosylated"
FT Modified-site 213
FT /note= "N-glycosylated"
FT Modified-site 261
FT /note= "N-glycosylated"
FT Modified-site 280
FT /note= "N-glycosylated"
FT Modified-site 328
FT /note= "N-glycosylated"
FT Modified-site 372
FT /note= "N-glycosylated"
FT Modified-site 503
FT /note= "putative autophosphorlation and substrate
FT binding site"
FT Modified-site 736
FT /note= "putative autophosphorlation and substrate
FT binding site"
FT Modified-site 740
FT /note= "putative autophosphorlation and substrate
FT binding site"
FT Modified-site 741
FT /note= "putative autophosphorlation and substrate
FT binding site"
FT Modified-site 813
FT /note= "putative autophosphorlation and substrate
FT binding site"
FT Modified-site 825
FT /note= "putative autophosphorlation and substrate
FT binding site"
FT Region 400..421
FT /label= transmembrane_region
FT /note= "putative"
FT Domain 30..185
FT /label= Discoidin_I_like_domain
FT Binding-site 433..438
FT /label= protein_kinase_C_binding_site
FT /note= "putative"
XX
PN US5677144-A.
XX
PD 14-OCT-1997.
XX
PF 08-NOV-1994; 94US-0336343.
XX
PR 16-NOV-1993; 93US-0153397.
XX
PA (ALVE/) ALVES F H E.
PA (ULLR/) ULLRICH A.
XX
PI Alves FHE, Ullrich A;
XX
DR WPI; 1997-511869/47.
DR N-PSDB; AAT93784.
XX
PT Truncated receptor tyrosine kinase CCK-2 - and nucleic acid coding
PT for it, useful for cancer diagnosis
XX
PS Claim 5; Fig 3; 70pp; English.
XX
CC The present sequence represents the amino acid sequence of human CCK-2,
CC a member of the mammary carcinoma kinase 10 (MCK-10, AAW34672) family of
CC receptor tyrosine kinases. The protein contains a remarkably high
CC number of proline residues arranged as PXXP or PXXXP repeats, suggesting
CC a random coil structure for the hydrophilic juxtamembrane region. This
CC region is probably a major domain for interactions with cellular
CC substrates and other regulatory proteins. Expression of CCK-2 is
CC associated with proliferative diseases such as cancer. The CCK-2 gene
CC was identified by PCR and a cDNA prepared from colonic adenocarcinoma
CC RNA. CCK-2 is expressed in a wide variety of cancer cell lines and
CC tumour tissue. The CCK-2 nucleic acids can be used for diagnostic
CC purposes to detect aberrant expression of CCK-2 genes. Engineered cell

CC lines, containing recombinant vectors with the present sequence, are
CC useful for producing infectious retroviral particles. The cell lines may
CC also be used to evaluate and screen drugs involved in CCK-2 activation
CC and regulation.
XX
SQ Sequence 855 AA;

Query Match 48.8%; Score 2404; DB 18; Length 855;
Best Local Similarity 51.8%; Pred. No. 5.7e-176;
Matches 482; Conservative 118; Mismatches 227; Indels 104; Gaps 16;

```
Qy       3 PEALSSLLLLLLVASGDADMKGHFDPAKCRYALGMQDRTIPDSDISASSSWSDSTAARHS 62
Db       5 prmllvlfllpils---sakaqvnpaicryplgmsgggipdeditassqwsestaakyg 61

Qy      63 RLESSDGDGAWCPAGSVFPKE-EEYLQVDLQRLHLVALVGTQGRHAGGLGKEFSRSYRLR 121
Db      62 rldseegdgawcpeipvepddlkeflqidlhtlhfitlvgtqgrhagghgiefapmykin 121

Qy     122 YSRDGRRWMGWKDRWGQEVISGNEDPEGVVLKDLGPPMVARLVRFYPRADRVMSVCLRVE 181
Db     122 ysrdgtrwiswrnrhgkqvldgnsnpydiflkdleppivarfvrfipvtdhsmnvcmrve 181

Qy     182 LYGCLWRDGLLSYTAPVGQTMYL--SEAVYLNDSTYDGHTVGGLQYGGLGQLADGVVGLD 239
Db     182 lygcvwldglvsynapagqqfvlpggsiiylndsvydg-avgysmteglgqltdgvsgld 240

Qy     240 DFRKSQELRVWPGYDYVGWSNHSFSSGYVEMEFEFDRLRAFQAMQVHCNNMHTLGARLPG 299
Db     241 dftqtheyhvwpgydyvgwrnesatngyieimfefdrirnfttmkvhcnnmfakgvkifk 300

Qy     300 GVECRFRRGPAMAWEGEPMRHNLGGNLGDPRARAVSVPLGGRVARFLQCRFLFAGPWLLF 359
Db     301 evqcyf-rseasewepnaisfplvlddvnpsarfvtvplhhrmasaikcqyhfadtwmmf 359

Qy     360 SEISFISD-VVNNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTAI 418
Db     360 seitfqsdaamynnseal----ptsp--------------mapttydpmlkvddsntri 400

Qy     419 LIGCLVAIILLLLLLIIALMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTILINNR--P 476
Db     401 ligclvaiifillaiiviilwrqfwqkmlekasrrmlddemtvslslpsdssmfnnnrss 460

Qy     477 GPREP------------PPYQEPRPRGNPPHSAPCVPNGSALLLSNPAYRLLLATYARP 523
Db     461 spseqgsnstydrifplrpdyqep---------------srlirklpef---------- 494

Qy     524 PRGPGPPTPAWAKPTNTQAYSGDYMEPEKPGAPLLPPPPQNSVPHYAEADIVTLQGVTGG 583
Db     495 ------------apgeeesgcsgvvkpvqpsgp-------egvphyaeadivnlqgvtgg 535

Qy     584 NTYAVPALPPGAVGDGPPRV-DFPRSRLRFKEKLGEGQFGEVHLCEVDSPQDLVSLDFPL 642
Db     536 ntysvpavtmdllsgkdvaveefprkllfkeklgegqfgevhlcevegmekfkdkdfal 595

Qy     643 NVRKGHPLLVAVKILRPDATKNASFSLFSRNDFLKEVKIMSRLKDPNIIRLLGVCVQDDP 702
Db     596 dvsanqpvlvavkmlradankna------rndflkeikimsrlkdpniihllsvcitddp 649

Qy     703 LCMITDYMENGDLNQFLSAHQLEDKAAEGAPGDGQAAQGPTISYPMLLHVAAQIASGMRY 762
Db     650 lcmiteymengdlnqflsrhe---------ppnssssdvrtvsytnlkfmatqiasgmky 700

Qy     763 LATLNFVHRDLATRNCLVGENFTIKIADFGMSRNLYAGDYYRVQGRAVLPIRWMAWECIL 822
Db     701 lsslnfvhrdlatrnclvgknytikiadfgmsrnlysgdyyriqgravlpirwmswesil 760

Qy     823 MGKFTTASDVWAFGVTLWEVLMLCRAQPFGQLTDEQVIENAGEFFRDQGRQVYLSRPPAC 882
Db     761 lgkfttasdvwafgvtlwetftfcqeqpysqlsdeqvientgeffrdqgrqtylpqpaic 820

Qy     883 PQGLYELMLRCWSRESEQRPPFSQLHRFLAE 913
```

```
Db     821 pdsvyklmlscwrrdtknrpsfqeihllllq 851
```

RESULT 13
AAW77114
ID AAW77114 standard; Protein; 855 AA.
XX
AC AAW77114;
XX
DT 16-NOV-1998 (first entry)
XX
DE Discoidin domain receptor 2 protein.
XX
KW Discoidin domain receptor; transformation; metastasis; collagen; ss;
KW Cleidocranial displasia; Sickler syndrome; extracellular matrix; MMP-1.
XX
OS Homo sapiens.
XX
PN WO9834954-A2.
XX
PD 13-AUG-1998.
XX
PF 05-FEB-1998; 98WO-CA00093.
XX
PR 06-FEB-1997; 97US-0041578.
XX
PA (MOUN) MOUNT SINAI HOSPITAL CORP.
XX
PI Pawson A, Vogel W;
XX
DR WPI; 1998-447168/38.
DR N-PSDB; AAV48292.
XX
PT Novel ligands of discoidin domain receptor tyrosine kinase,
PT especially collagen - useful for treating e.g. metastasis,
PT cleidocranial displasia or Sickler syndrome
XX
PS Disclosure; Fig 22a; 115pp; English.
XX
CC The discoidin domain receptor (DDR) can be used to identify and evaluate
CC substances which affect DDR receptor tyrosine kinase signalling pathways
CC in the cell. Compounds which modulate such signalling pathways can be
CC used to alter transformation or metastasis in mammals, to treat
CC conditions involving structural or functional deregulation of collagens,
CC e.g. Cleidocranial displasia or Sickler syndrome, conditions requiring
CC modulation of extracellular matrix synthesis, degradation or remodelling,
CC or to treat conditions needing modulation of MMP-1 expression such as
CC wound healing.
XX
SQ Sequence 855 AA;

Query Match 48.8%; Score 2404; DB 19; Length 855;
Best Local Similarity 51.8%; Pred. No. 5.7e-176;
Matches 482; Conservative 118; Mismatches 227; Indels 104; Gaps 16;

```
Qy       3 PEALSSLLLLLLVASGDADMKGHFDPAKCRYALGMQDRTIPDSDISASSSWSDSTAARHS 62
Db       5 prmllvlfllpils---sakaqvnpaicryplgmsgggipdeditassqwsestaakyg 61

Qy      63 RLESSDGDGAWCPAGSVFPKE-EEYLQVDLQRLHLVALVGTQGRHAGGLGKEFSRSYRLR 121
Db      62 rldseegdgawcpeipvepddlkeflqidlhtlhfitlvgtqgrhagghgiefapmykin 121

Qy     122 YSRDGRRWMGWKDRWGQEVISGNEDPEGVVLKDLGPPMVARLVRFYPRADRVMSVCLRVE 181
Db     122 ysrdgtrwiswrnrhgkqvldgnsnpydiflkdleppivarfvrfipvtdhsmnvcmrve 181

Qy     182 LYGCLWRDGLLSYTAPVGQTMYL--SEAVYLNDSTYDGHTVGGLQYGGLGQLADGVVGLD 239
Db     182 lygcvwldglvsynapagqqfvlpggsiiylndsvydg-avgysmteglgqltdgvsgld 240
```

```
Qy    240 DFRKSQELRVWPGYDYVGWSNHSFSSGYVEMEFEFDRLRAFQAMQVHCNNMHTLGARLPG 299
          || :: |  |||||||||| | | ::||:|: |||||:| |  |:||||||   | ::
Db    241 dftqtheyhvwpgydyvgwrnesatngyieimfefdrirnfttmkvhcnnmfakgvkifk 300

Qy    300 GVECRFRRGPAMAWEGEPMRHNLGGNLGDPRARAVSVPLGGRVARFLQCRFLFAGPWLLF 359
          |:| | |  |  ||   :  |  :  :| || |:|||  |:|  ::|:: ||  |::|
Db    301 evqcyf-rseasewepnaisfplvlddvnpsarfvtvplhhrmasaikcqyhfadtwmmf 359

Qy    360 SEISFISD-VVNNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTAI 418
          |||:| ||  : |:| ||   | :|              : |    |: | : | | |
Db    360 seitfqsdaamynnseal----ptsp--------------mapttydpmlkvddsntri 400

Qy    419 LIGCLVAIILLLLLIIALMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTILINNR--P 476
          |||||||| :|| || ::||| |:::| || ||:|::|:|| ||:| |: : ||
Db    401 ligclvaiifillaiiviilwrqfwqkmlekasrrmlddemtvslslpsdssmfnnnrss 460

Qy    477 GPREP------------PPYQEPRPRGNPPHSAPCVPNGSALLLSNPAYRLLLATYARP 523
          | |              | ||||              | |:   | :
Db    461 spseqgsnstydrifplrpdyqep---------------srlirklpef---------- 494

Qy    524 PRGPGPPTPAWAKPTNTQAYSGDYMEPEKPGAPLLPPPPQNSVPHYAEADIVTLQGVTGG 583
                    |   ::     ::| :|  |          |||||||||| |||||||
Db    495 -----------apgeeesgcsgvvkpvqpsgp-------egvphyaeadivnlqgvtgg 535

Qy    584 NTYAVPALPPGAVGDGPPRV-DFPRSRLRFKEKLGEGQFGEVHLCEVDSPQDLVSLDFPL 642
          |||:|||:    :     | :|||  | |||||||||||||||||:  :     || |
Db    536 ntysvpavtmdllsgkdvaveefprklltfkeklgegqfgevhlcevegmekfkdkdfal 595

Qy    643 NVRKGHPLLVAVKILRPDATKNASFSLFSRNDFLKEVKIMSRLKDPNIIRLLGVCVQDDP 702
          :|    |:|||||:|| || |||      |||||||:|||||||||||| || ||: |||
Db    596 dvsanqpvlvavkmlradankna------rndflkeikimsrlkdpniihllsvcitddp 649

Qy    703 LCMITDYMENGDLNQFLSAHQLEDKAAEGAPGDGQAAQGPTISYPMLLHVAAQIASGMRY 762
          |||||:|||||||||| |:         | :  ::   |:||  |  :| ||||||:|
Db    650 lcmiteymengdlnqflsrhe---------ppnssssdvrtvsytnlkfmatqiasgmky 700

Qy    763 LATLNFVHRDLATRNCLVGENFTIKIADFGMSRNLYAGDYYRVQGRAVLPIRWMAWECIL 822
          |::|||||||||||||||:|:|||||||||||||:|||||:|||||||||||:|| ||
Db    701 lsslnfvhrdlatrnclvgknytikiadfgmsrnlysgdyyriqgravlpirwmswesil 760

Qy    823 MGKFTTASDVWAFGVTLWEVLMLCRAQPFGQLTDEQVIENAGEFFRDQGRQVYLSRPPAC 882
          :|||||||||||||||||    |: ||: ||:|||||| |||||||||| || :|  |
Db    761 lgkfttasdvwafgvtlwetftfcqeqpysqlsdeqvientgeffrdqgrqtylpqpaic 820

Qy    883 PQGLYELMLRCWSRESEQRPPFSQLHRFLAE 913
          |  :|:||| || |::: || | ::|  | :
Db    821 pdsvyklmlscwrrdtknrpsfqeihllllq 851
```

```
RESULT  14
AAW79152
ID   AAW79152 standard; Protein; 854 AA.
XX
AC   AAW79152;
XX
DT   19-NOV-1998  (first entry)
XX
DE   Receptor protein tyrosine kinase (PTK) subtype tyro-10.
XX
KW   PTK; receptor; protein tyrosine kinase; brain tissue.
XX
OS   Rattus sp.
XX
PN   US5811516-A.
XX
PD   22-SEP-1998.
XX
PF   02-JUN-1995;   95US-0456647.
XX
PR   15-MAY-1992;   92US-0884486.
PR   02-MAY-1994;   94US-0237401.
PR   02-JUN-1995;   95US-0456647.
XX
PA   (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
PI   Lai CHC,  Lemke GE;
XX
DR   WPI; 1998-530939/45.
DR   N-PSDB; AAV55895.
XX
PT   Receptor protein tyrosine kinase polypeptide, tyro-3 - preferably
PT   expressed in brain tissue
XX
PS   Example 2; Columns 53-60; 46pp; English.
XX
CC   This represents a novel receptor protein tyrosine kinase (PTK)
CC   polypeptide subtype tyro-10. The invention provides polynucleotide
CC   sequences encoding novel PTK polypeptide subtypes tyro-1 to tyro-13.
CC   The PTK subtypes are found expressed predominantly in the brain tissue.
XX
SQ   Sequence   854 AA;
```

```
  Query Match           48.7%;  Score 2402;  DB 19;  Length 854;
  Best Local Similarity  51.9%;  Pred. No. 8e-176;
  Matches  481;  Conservative  119;  Mismatches  220;  Indels  106;  Gaps   16;

Qy      9 LLLLLLVASGDADMKGHFDPAKCRYALGMQDRTIPDSDISASSSWSDSTAARHSRLESSD 68
          :|||||:  | |  |   :|| ||| |||    ||| ||:||| ||:|||||: ||:| :
Db     10 vlllllllgsa--kaqvnpaicryplgmsgghipdeditassqwsestaakygrldsee 67

Qy     69 GDGAWCPAGSVFPKE-EEYLQVDLQRLHLVALVGTQGRHAGGLGKEFSRSYRLRYSRDGR 127
          |||||||   | | : :|:||:||: || : |||||||||| | ||:  |:: |||||
Db     68 gdgawcpeipvqpddlkeflqidlrtlhfitlvgtqgrhagghgiefapmykinysrdgs 127

Qy    128 RWMGWKDRWGQEVISGNEDPEGVVLKDLGPPMVARLVRFYPRADRVMSVCLRVELYGCLW 187
          ||: |::| |::|: || :|  | |||| ||:||| || ,|  | |:||:|||||||:|
Db    128 rwiswrnrhgkqvldgnsnpydvflkdleppivarfvrlipvtdhsmnvcmrvelygcvw 187

Qy    188 RDGLLSYTAPVGQTMYL--SEAVYLNDSTYDGHTVGGLQYGGLGQLADGVVGLDDFRKSQ 245
          |||:|| || ||   |     :||||| ||| ||     ||||| ||| ||||| ::
Db    188 ldglvsynapagqqfvlpggsiiylndsvydg-avgysmteglgqltdgvsglddftqth 246

Qy    246 ELRVWPGYDYVGWSNHSFSSGYVEMEFEFDRLRAFQAMQVHCNNMHTLGARLPGGVECRF 305
          |  ||||||||| | | ::|::|: ||||||:| |  |:||||||   | ::   |:| |
Db    247 eyhvwpgydyvgwrnesatngfieimfefdrirnfttmkvhcnnmfakgvkifkevqcyf 306

Qy    306 RRGPAMAWEGEPMRHNLGGNLGDPRARAVSVPLGGRVARFLQCRFLFAGPWLLFSEISFI 365
          |  |  ||   :  |  :  :| || |:|||  |:|  ::|:: ||  |::|||||:|
Db    307 -rseaseweptavyfplvlddvnpsarfvtvplhhrmasaikcqyhfadtwmmfseitfq 365

Qy    366 SD--VVNNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTAILIGCL 423
          ||  : |||     |  | :|               : |    |: | : | | ||||||
Db    366 sdaamynns-----galptsp--------------mapttydpmlkvddsntriligcl 405

Qy    424 VAIILLLLLIIALMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTILINNR----PGPR 479
          |||| :|| || ::|||  |:::| || ||:|::|:|| ||:| :: : ||     | :
Db    406 vaiifillaiiviilwrqfwqkmlekasrrmlddemtvslslpsessmfnnnrssspseq 465

Qy    480 EP-----------PPYQEPRPRGNPPHSAPCVPNGSALLLSNPAYRLLLATYARPPRGPG 528
          |            | ||||              | |:   | :
Db    466 esnstydrifplrpdyqep---------------srlirklpef---------------- 494

Qy    529 PPTPAWAKPTNTQAYSGDYMEPEKPGAPLLPPPPQNSVPHYAEADIVTLQGVTGGNTYAV 588
                  |   ::     ::| :|  |          |||||||||| |||||||||| |
Db    495 -------apgeeesgcsgvvkpaqpngp-------egvphyaeadivnlqgvtggntycv 540

Qy    589 PALPPGAVGDGPPRV-DFPRSRLRFKEKLGEGQFGEVHLCEVDSPQDLVSLDFPLNVRKG 647
          ||:    :       | :|||  | |||||||||||||||||:  :     || |:|
Db    541 pavtmdllsgkdvaveefprkllafkeklgegqfgevhlcevegmekfkdkdfaldvsan 600

Qy    648 HPLLVAVKILRPDATKNASFSLFSRNDFLKEVKIMSRLKDPNIIRLLGVCVQDDPLCMIT 707
          |:|||||:|| ||·|||      |||||||:|||||||||||||| ||: :|||||||
Db    601 qpvlvavkmlradankna------rndflkeikimsrlkdpniirllavcitedplcmit 654

Qy    708 DYMENGDLNQFLSAHQLEDKAAEGAPGDGQAAQGPTISYPMLLHVAAQIASGMRYLATLN 767
```

```
Db    655 eymengdlnqflsrheplsscssda----------tvsyanlkfmatqiasgmkylssln 704

Qy    768 FVHRDLATRNCLVGENFTIKIADFGMSRNLYAGDYYRVQGRAVLPIRWMAWECILMGKFT 827
Db    705 fvhrdlatrnclvgknytikiadfgmsrnlysgdyyriqgravlpirwmswesillgkft 764

Qy    828 TASDVWAFGVTLWEVLMLCRAQPFGQLTDEQVIENAGEFFRDQGRQVYLSRPPACPQGLY 887
Db    765 tasdvwafgvtlwetftfcqeqpysqlsdeqvientgeffrdqgrqiylpqpalcpdsvy 824

Qy    888 ELMLRCWSRESEQRPPFSQLHRFLAE 913
Db    825 klmlscwrretkhrpsfqeihllllq 850
```

RESULT 15
AAW81409
ID AAW81409 standard; Protein; 854 AA.
XX
AC AAW81409;
XX
DT 22-JAN-1999 (first entry)
XX
DE Receptor protein tyrosine kinase (PTK) subtype tyro-10.
XX
KW PTK; receptor; protein tyrosine kinase; recombinant; grafting;
KW diagnosis; tumour; skin transplant; connective tissue; tyro-10.
XX
OS Rattus sp.
XX
PN US5837448-A.
XX
PD 17-NOV-1998.
XX
PF 02-MAY-1994; 94US-0237401.
XX
PR 15-MAY-1992; 92US-0884486.
PR 02-MAY-1994; 94US-0237401.
XX
PA (SALK) SALK INST BIOLOGICAL STUDIES.
XX
PI Lai CHC, Lemke GE;
XX
DR WPI; 1999-023436/02.
DR N-PSDB; AAV65317.
XX
PT Nucleic acids encoding protein tyrosine kinase sub:types - for
PT identification of new sub:types and treatment of diseases associated
PT with the kinase
XX
PS Claim 10; Columns 53-58; 47pp; English.
XX
CC This represents a receptor protein tyrosine kinase (PTK) subtype
CC tyro-10. The invention provides sequences AAV65308 to AAV65313, AAV65315,
CC and AAV65317 to AAV65319 that encode proteins having a tyrosine kinase
CC domain and a tissue expression pattern of a receptor PTK subtype selected
CC from tyro-1, tyro-2, tyro-3, tyro-4, tyro-5, tyro-6, tyro-8, tyro-10,
CC tyro-11, and tyro-12, respectively. The polynucleotides are useful for
CC the detection of tyrosine kinase domain sequences and detection of tissue
CC expression patterns of PTK subtypes. The cDNAs can also be injected into
CC oocytes, the protein expressed, and expression products screened for
CC using antibodies against tyrosine kinase epitopes. These subtypes
CC sequences can be used for the design of oligonucleotides, for use in
CC amplification reactions to isolate other subtype sequences. These
CC detection protocols are used in the diagnosis of diseases associated with
CC (receptor) PTKs. Recombinant vectors expressing the subtypes can be used
CC to treat related diseases e.g. tumours, by introduction of the vectors
CC into skin transplants, then grafting these into the connective tissue of
CC the dermis, thus specifically targetting tumours as the proteins are
CC released from the matrix.
XX
SQ Sequence 854 AA;

Query Match 48.7%; Score 2402; DB 20; Length 854;
Best Local Similarity 51.9%; Pred. No. 8e-176;
Matches 481; Conservative 119; Mismatches 220; Indels 106; Gaps 16;

```
Qy      9 LLLLLLVASGDADMKGHFDPAKCRYALGMQDRTIPDSDISASSSWSDSTAARHSRLESSD 68
Db     10 vlllllllgsa--kaqvnpaicryplgmsgghipdeditassqwsestaakygrldsee 67

Qy     69 GDGAWCPAGSVFPKE-EEYLQVDLQRLHLVALVGTQGRHAGGLGKEFSRSYRLRYSRDGR 127
Db     68 gdgawcpeipvqpddlkeflqidlrtlhfitlvgtqgrhagghgiefapmykinysrdgs 127

Qy    128 RWMGWKDRWGQEVISGNEDPEGVVLKDLGPPMVARLVRFYPRADRVMSVCLRVELYGCLW 187
Db    128 rwiswrnrhgkqvldgnsnpydvflkdleppivarfvrlipvtdhsmnvcmrvelygcvw 187

Qy    188 RDGLLSYTAPVGQTMYL--SEAVYLNDSTYDGHTVGGLQYGGLGQLADGVVGLDDFRKSQ 245
Db    188 ldglvsynapagqqfvlpggsiiylndsvydg-avgysmteglgqltdgvsglddftqth 246

Qy    246 ELRVWPGYDYVGWSNHSFSSGYVEMEFEFDRLRAFQAMQVHCNNMHTLGARLPGGVECRF 305
Db    247 eyhvwpgydyvgwrnesatngfieimfefdrirnfttmkvhcnnmfakgvkifkevqcyf 306

Qy    306 RRGPAMAWEGEPMRHNLGGNLGDPRARAVSVPLGGRVARFLQCRFLFAGPWLLFSEISFI 365
Db    307 -rseaseweptavyfplvlddvnpsarfvtvplhhrmasaikcqyhfadtwmmfseitfq 365

Qy    366 SD--VVNNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTAILIGCL 423
Db    366 sdaamynns-----galptsp--------------mapttydpmlkvddsntriligcl 405

Qy    424 VAIILLLLLLIIALMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTILINNR----PGPR 479
Db    406 vaiifillaiiviilwrqfwqkmlekasrrmlddemtvslslpsessmfnnnrsssspseq 465

Qy    480 EP-----------PPYQEPRPRGNPPHSAPCVPNGSALLLSNPAYRLLLATYARPPRGPG 528
Db    466 esnstydrifplrpdyqep---------------srlirklpef--------------- 494

Qy    529 PPTPAWAKPTNTQAYSGDYMEPEKPGAPLLPPPPQNSVPHYAEADIVTLQGVTGGNTYAV 588
Db    495 -------apgeeesgcsgvvkpaqpngp-------egvphyaeadivnlqgvtggntycv 540

Qy    589 PALPPGAVGDGPPRV-DFPRSRLRFKEKLGEGQFGEVHLCEVDSPQDLVSLDFPLNVRKG 647
Db    541 pavtmdllsgkdvaveefprkllafkeklgegqfgevhlcevegmekfkdkdfaldvsan 600

Qy    648 HPLLVAVKILRPDATKNASFSLFSRNDFLKEVKIMSRLKDPNIIRLLGVCVQDDPLCMIT 707
Db    601 qpvlvavkmlradankna------rndflkeikimsrlkdpniirllavcitedplcmit 654

Qy    708 DYMENGDLNQFLSAHQLEDKAAEGAPGDGQAAQGPTISYPMLLHVAAQIASGMRYLATLN 767
Db    655 eymengdlnqflsrheplsscssda----------tvsyanlkfmatqiasgmkylssln 704

Qy    768 FVHRDLATRNCLVGENFTIKIADFGMSRNLYAGDYYRVQGRAVLPIRWMAWECILMGKFT 827
Db    705 fvhrdlatrnclvgknytikiadfgmsrnlysgdyyriqgravlpirwmswesillgkft 764

Qy    828 TASDVWAFGVTLWEVLMLCRAQPFGQLTDEQVIENAGEFFRDQGRQVYLSRPPACPQGLY 887
Db    765 tasdvwafgvtlwetftfcqeqpysqlsdeqvientgeffrdqgrqiylpqpalcpdsvy 824

Qy    888 ELMLRCWSRESEQRPPFSQLHRFLAE 913
Db    825 klmlscwrretkhrpsfqeihllllq 850
```

Search completed: October 4, 2002, 07:40:41

Job time: 261 sec